

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm ch_nn

Tue Dec 15 18:30:42 1998; MasPar time 1134.44 Seconds 1365.449 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-109-864-1 (1-865) from US09109864.seq 865 Title: Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 •• STD Nmatch

2275026 seqs, 895388244 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est55 Database:

Database:

5:qb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13 10:gb_est14 11:gb_est15 12:gb_est16 11:gb_est17 14:gb_est18 15:gb_est18 15:gb_est2 17:gb_est2 10:gb_est2 10:gb_est2 11:gb_est2 11:gb_est2 11:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6 21:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2 28:gb_gss3 29:gb_gss4 1:em_estl 2:em_gssl 3:em_gss2 4:em_gss3 genbank-estl07

Mean 12.059; Variance 7.331; scale 1.645 Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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æ	Query	53.5	38.8	36.9	25.5	13.9	9.5	7.1	6.4	5.9	5.8	5.8	5.7	5.7
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ALIGNMENTS

AA311108 496 bp mRNA EST 19-APR-1997 EST181872 Jurkat T-cells V Homo sapiens CDNA 5' end, mRNA sequence. AA311108 g1963435 EST. human. Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	daans, M.D., Karlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Adans, M.D., Karlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Adans, M.D., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzchugh, W.M., Fritchman, J.L., Geophagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. Jr., Kelley, J.C., Liu, L. I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudey, D.M., Shriey, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, DF., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudsson, P., Kim, A.K., Rozak, D.L., Kunsch, C., Hugyjun, J., Li, H., Meissner, P.S., Olsen, H., Fraser, C. M. and Verter, R. Rosen, C.A., Haseltine, M.A., Fields, C., Fraser, C. M. and Verter, T. Rozen, C.A., Haseltine, M.A., Fields, C.,	Initial assessment of human gene diversity and expression patterns "Dased upon 83 million nucleotides of cDNA sequence
RESULT 1 LOCUS LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE

Nature 377 (6547 Suppl), 3-174 (1995) 96026280 The Institute for Genomic Research Other ESTs: THC124424 Contact: Kerlavage, AR Bioinformatics JOURNAL MEDITINE

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                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi.html) seq primer: M13 Reverse.
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9712 Medical Center Drive, Rockville, MD 20850 USA
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Pred. No. 2.06e-287;
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares
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Barcopterygii; Chonata; Vertebrata; Gnathostomata; Theria;

Butheria; Archonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonata; Tetrapoda; Amniota; Hominidae; Homo.

[ (bases 1 to 411)

Hillier, L., Clark, N., Dubnque, T., Elliston, K., Hawkins, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stops: 264 Source: IMAGE Consortium, LLNL this clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-Merck EST Project
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 15 15:55:11 1998; MasPar time 5.67 Seconds 629.394 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-109-864-2 (1-133) from US09109864.pep 980 1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133 Title: Description: Perfect Score: Sequence:

Scoring table:

74019 seqs, 26840295 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot35 1:swissprot Database:

Mean 44.065; Variance 78.778; scale 0.559 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.71e-14	2.88e-09	3.11e-08	3.11e-08	1.49e-07	9.88e-06	1.12e-03	1.12e-03	3.21e-03	3.21e-03	9.03e-03	9.41e-02	1.30e-01	1.80e-01	3.42e-01	4.70e-01	6.43e - 01	6.43e - 01	8.79e-01	8.79e-01	8.79e-01	1.63e+00	1.63e+00
Description	GALECTIN-5 (RL-18).	GALECTIN-9 (36 KD BETA	GALECTIN-8 (PROSTATE C	GALECTIN-9.	GALECTIN-7 (HKL-14).	GALECTIN-9 (HOM-HD-21)	32 KD BETA-GALACTOSIDE	PROBABLE 33 KD BETA-GA	GALECTIN-8 (30 KD S-TY	GALECTIN-4 (LACTOSE-BI	UDP-N-ACETYLGLUCOSAMIN	BETA-GALACTOSIDE-BINDI	COPPER TRANSPORT ATP-B	HYPOTHETICAL 21.0 KD P	FERRIC ENTEROBACTIN RE	GALECTIN-7.	PROBABLE GENERAL SECRE	SODIUM CHANNEL PROTEIN	PREPROTEIN TRANSLOCASE	COMPLEMENT FACTOR I PR	GLUTATHIONE-REGULATED	MULTIDRUG RESISTANCE P	COENZYME PQQ SYNTHESIS
ΩI	LEG5_RAT	LEG9 RAT	LEG8_HUMAN	LEG9_MOUSE	LEG7_HUMAN	LEG9_HUMAN	LE32_CAEEL	LE33_CAEEL	LEG8_RAT	LEG4_RAT	GPT_YEAST	LEG4_CHICK	NOSF_PSEST	YRNA_CAEEL	PFEA_PSEAE	LEG7_RAT	GSPE_ECOLI	CIN1_LOLBL	SECY_STRGR	CFAI_HUMAN	KEFC_ECOLI	EMRB_HAEIN	PQOF_KLEPN
DB	; -	Н	٦	-	Н	-	Н	Н	Н	Н	Н	Н	-	П	Н	-	-	ч	-	Н	-	Н	-
Query Match Length	144	354	316	353	135	355	279	289	316	324	448	134	308	184	746	135	493	1522	437	583	620	510	761
Query Match	17.8	14.9	14.3	14.3	13.9	12.8	11.4	11.4	11.1	11.1	10.8	10.1	10.0	o.	9.7	9.6	9.5	9.5	9.4	9.4	9.4	9.5	9.5
Score	174	146	140	140	136	125	112	112	109	109	106	66	98	97	95	94	93	93	92	92	92	90	90
Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

2.21e+000 2.21e+000 2.21e+000 2.21e+000 2.31e+000 2.38e+000 4.02e+000 4.02e+000 4.02e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000 7.24e+000		Gaps 6; vvr 68 :: .: LAW 62 LPD 127 LEQ 116
GLOBAL NITROGEN REGULA GALECTIN-4 (LACTOSE-BI HYDOTHETICAL PROTEIN C. FIBER PROTEIN C. SULKITE REDUCTASE, ASS COAT PROTEIN (CAPSID P SETAPTERIN REDUCTASE D NA POLYMERASE III, DE HYDOTHETICAL R6.8 KD P DNA-DIRECTED RNA POLYM ENDOGLUCANASE A PRECUR HYDOXYATRAZINE HYDROL GLOBAL NITROGEN REGULA GALECTIN-3 (GALACTOSE- MODIFICATION METHLASE NOUPLECATION METHLASE MENA CAPPING ALPHA-MANNOSIDASE I PRECUR	UPDATE) ON UPDATE) ON UPDATE) CON UPDATE) BRATA; TETRAPODA; MAMMALIA; UENCE. J., BARONDES S.H.; FOCTTE DIFFERENTIATION. S. PTIN (S-LECTIN) FAMILY. E; 1.	tch 17.8%; Score 174; DB 1; Length 144; al Similarity 28.0%; Pred. No. 2.71e-14; 37; Conservative 38; Mismatches 49; Indels 8; Ga PNLAVPFFTSIPNGLYPSKSIVISGVVLSDAKRFQINLRC-GGDIAFHLNPRFDENAVVR
NTCA_SINY3 LEG4_HUMAN FIEDA_BEBBB SCB_VEREN STR_DESVH COAT_BEBNY SPRE_BAT HOLA_ECOLI REO_COXTSA RPOD_MAIZE GUNA_CALSA ATZB_PESSE NTCA_ANASP INTCA_ANASP INTCA_ANAS	ACE ATIO	SCOTE 174; Pred. No. 2 38; Mismat VISGVVLSDAKRF :: : :: : IVRGLVLQEPKHF SRGQRF-SVWILC : YP-QRFFEVLLLF
225 325 325 1936 1976 1976 1152 1152 1152 1152 1152 1152 1152 1162 116	S 254 CB B 185 185 185 28 65	tch al Similarity 28.0%; Pred 37; Conservative 38; PNLAVPETSIPNGLYPSKSIVISGVV
00000000000000000000000000000000000000	AT STAN 1-1996 (REL. 3 1-199	tch al Similarity 28, 37; Conservati) PNLAVPEFTSIPNGLYPS FILE
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	LEG5_RAT STANDAJ P47967; 01-FEB1996 (REL. 33, 01-FEB196 (REL. 34, 01-FEB196	
	RESULT LEG AC P470 DT O1-100 DT O1-1	Ouery Marches Matches Db 10 Oy 3 Db 69 Oy 63 Oy 63
	T.	

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GALECTIN-9.
LEG8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                  LGALS8
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ABRAMSON R.G.;
J. BIOL. CHEM. 272:617-625(1997). MAY PLAY A ROLE IN THYMOCYTE-
1- FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
PETHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS (BY EDITHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS (BY EDITHARITY). MAY PROVIDE THE MOLECULAR BASIS FOR URATE FLUX ACROSS CELL MEMBRANES, ALLOWING URATE THAT IS FORMED DURING PURINE METABOLISM TO EFFLUX FROM CELLS AND SERVING AS AN ELECTROGENIC TRANSPORTER THAT PLAYS AN IMPORTANT ROLE IN RENAL AND GASTROINTESTINAL URATE EXCRETION. HIGHLY SELECTIVE TO THE ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSICAL SECRETORY PATHWAY (BY SIMILARITY).
--- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED BY
ALTERNATIVE SPLICING. THE LONG FORM (SHOWN HERE) IS EXPRESSED
EXCLUSIVELY IN THE SMALL INTESTINE.
--- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 RNTQINNSWGPEERSLPGRMPFNRGQSFSVWILCEGHCFKVAVDGQHICEYYHRLKNLPD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 TPAYIIPFFTSIPNGFYPSKSINISGVVLPDAKRFHINLRC-GGDIAFHLNPRFNEKVVV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT FORM).
STRAIN-SPRAGUE-DAWLEY; IISSUE-KIDNEY;
LEAL-PINTO E., TAO W., RAPPAPORT J., RICHARDSON M., KNORR B.A.,
                                                                                                                                                                                    RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILAMILI.
EMBL: U59462.; -(1916610; -.
EMBL: U72741: -; NOT_ANNOTATED_CDS.
EMBL: U67958; G1864095; -.
PROSITE; PS00309; LECTIN.GATACTOSIDE; 2.
GALAPTIN; LECTIN; REPEAT; ALTERNATIVE SPLICING; ION TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SHORT ISOFORM).
L -> H (IN REF. 2).
C7EB7FEA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
9
                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY, AND SWALL INTESTINE; MEDLINE; 97190351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 354;
                                                    P97840; 008588;
01-NOV-1997 (REL. 35, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECTIN-9 (36 KD BETA-GALACTOSIDE BINDING LECTIN) (URATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.88e-09;
                                      354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALAPTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 146;
                                                                                                                                                                                                                                                                                                                       WADA J., KANWAR Y.S.;
J. BIOL. CHEM. 272:6078-6086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39946 MW;
                                                                                                                                                     TRANSPORTER/CHANNEL) (UAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%;
Similarity 23.4%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | ::| :|| |::
117 LRELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 INTLEVAGDIQLTHVQT 354
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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286
148
187
                                    LEG9_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
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                                                                                                                                                                       LGALS9.
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Matches
                     RESULT
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179 TPQLSLPFAARLNTPMGPGRTVVVQGEVNANAKSFNVDLLAGKSKDIALHLNPRLNIKAF 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SPRLEVPCSHALPQGLSPGQVIIVRGLVLQEPRHFTVSL-RDQAAHAPVTLRASFADRTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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J. CLIN. INVEST. 99:2452-2461(1997).
-1- FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
EPITHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY).
EB4D9A3D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 140; DB 1; Length 316 Pred. No. 3.11e-08; 41; Mismatches 56; Indels
                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECTIN-8 (PROSTATE CARCINOMA TUMOR ANTIGEN) (PCTA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CD-1; TISSUE-SMALL INTESTINE, AND KIDNEY; MEDLINE; 97190351.
WADA J., KANWAR Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         008573; 008572;
01-NOV-1997 (REL. 35, CREATED)
11-NOV-1997 (REL. 35, LAST SEGUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AA.
   316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L78132; G1932712; -.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKER
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J. BIOL. CHEM. 272:6078-6086(1997).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALAPIIN; LECTIN; REPEAT; ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 SIDTLEINGDIHLLEVRS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.6%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 OLRELRISGSVOLYCVHS 133
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 3
248 2
316 AA;
                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN)
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96293510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97298141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE-PROSTATE
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TISSUE-SPLEEN
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                                                                                                        SEQUENCE
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                                                                                    INIT_MET
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
BINDING
                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                                                                                                                                                                                                                                                                   LGALS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                 Matches
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                         EMBRYO, DETECTED IN EMBRYONIC HEART, BRAIN, LUNG, LIVER, AND KIDNEY. HIGHLY EXPRESSED IN ADULT THYMUS, SMALL INTESTINE, AND KIDNEY. HIGHLY EXPRESSED IN ADULT THYMUS, SMALL INTESTINE, AND AND SKELETAL MUSCLE. BARELY DETECTABLE IN BRAIN AND RELICULOCYTE. DEVELOPMENTAL STAGE: THE EXPRESSION INCREASED WITH SUCCESSIVE ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING THE LONG FORM (SHOWN HERE) IS EXPRESSED EXCLUSIVELY IN THE SMALL INTESTINE.
                                                                                                                          -!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                       218 TPAYTIPFYTPIPNGLYPSKSIMISGNVLPDATRFHINLRC-GGDIAFHLNPRENENAVV 276
                                                                                                                                                                                                                                                                                                                                                                                RNTQINNSWGQEERSLLGRMPFSRGQSFSVWIICEGHCFKVAVNGQHMCEYYHRLKNLQD 336
                                                                                                                                                                                                                                                                                                                                                                                                  62 W---ISR-WGQK-KLISAPFLFYPQRFFEVLLLFQEGGLKLALNGQGLGATSMNQQALEQ 116
                    -!- TISSUE SPECIFICITY: ACCENTUATED EXPRESSION IN LIVER AND THYMUS OF
 SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 7-19; 75-82; 111-117 AND 120-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MADSEN P., RASMUSSEN H.H., FLINT T., GROMOV P., KRUSE T.A., HONORE I
VORUM H., CELIS J.E.;
J. BIOL. CHEM. 270:5823-5829(1995).
                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                           BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SHORT ISOFORM).
1AC8BAD75 CRC32;
                                                                                                                                              -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
EMBL; U55061; G1916604; -.
EMBL; U55060; G1916602; -.
                                                                                                                                                                                                                                                                                               Length 353;
                                                                                                                                                                                                                                                                                             Score 140, DB 1; Length 353
Pred. No. 3.11e-08;
40; Mismatches 58; Indels
                                                                                                                                                                           MGD; MGI:109496; LGALS9.
PROSITE; PSO0309; LECTIN_GALACTOSIDE; 2.
GALAPIN; LECTIN; REPEAT; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 AA.
                                                                                                                                                                                                            GALAPTIN 1.
                                                                                                                                                                                                                                GALAPTIN 2.
                                                                                                                                                                                                                       LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
          CLASSICAL SECRETORY PATHWAY
                                                                                                                                                                                                                                                                         40036 MW;
                                                                                                                                                                                                                                                                                             14.3%;
Similarity 24.1%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   : | ::| :| |::
117 LRELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                        337 INTLEVAGDIQLTHVQT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALECTIN-7 (HKL-14).
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-EPIDERMIS;
MEDLINE; 95197604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-EPIDERMIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 5
LEG7_HUMAN
P47929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY
                                                                                                                                                                                                                                                              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                               DOMAIN
BINDING
BINDING
                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGALS7
                                                                                                                                                                                                                                                                                                                                                                               277
                                                                                                                                                                                                                                                                                                                   Matches
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-!- FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
EPITHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS.
-!- TISSUE SPECIFICITY: PERIPHERAL BLOOD LEUKOCYTES AND LYMPHATIC
TISSUES. OVEREXPRESSED IN HODGKIN'S DISEASE TISSUE.
-!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NSKEQGSWGREERGPGVPFQR-GQPF-EVLIIASDDGFK-AVVGDAQYHHFRHRLPLARV 118
                                                                                                                                                                                                                                                                                                                                                                                                              :|| :||:|| || |: :|||| :: :| |:|
6 EVPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSL---RDQAAHAPVTLRASFADRTLAW 62
                                                                                                                                                                                                                                                                                                                                                                                   2 NVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVF 61
                                                                                                                                                                                                                                                                                                                                         Gaps
-!- TISSUE SPECIFICITY: MAINLY IN STRATIFIED SQUAMOUS EPITHELIUM.
                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SHORT ISOFORM).
K -> R (IN REF. 1).
S -> F (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97197815.
TUERECI O., SCHMITT H., FADLE N., PFREUNDSCHUH M., SAHIN U.;
J. BIOL. CHEM. 272:6416-6422(1997).
                                                                                                                                                                                                                                                                                        Score 136; DB 1; Length 135; Pred. No. 1.49e-07;
                                                                                                                                                                                                                BETA-GALACTOSIDE (POTENTIAL). 33656F93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- ALTERNATIVE PRODUCES: AT LEAST TWO FORMS ARE PRODUCED ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                      39; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LECTIN_GALACTOSIDE; 2.
REPEAT; ALTERNATIVE SPLICING.
148
GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEG9_HUMAN STANDARD; PRT; 355 AA. 000182; 014532; CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                   MIM; 600615; -.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
GALAPTIN; LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALAPTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                       135 AA; 14944 MW;
                                                                                             AARHUS/GHENT-2DPAGE; 17; IEF
                                                                                                                                                                                                                                                                                        13.9%;
                                                                                                                                                                                                                                                                                                           Local Similarity 28.1%;
les 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z49107; E310691; -.
EMBL; AB006782; D1023026;
                                            EMBL; L07769; G182132; -. EMBL; U06643; G458703; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-GASTRIC CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 RLVEVGGDVQLDSVR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : ::| ||| |:
118 RELRISGSVQLYCVH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALECTIN-9 (HOM-HD-21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206
355
88
2293
180
88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00309;
GALAPTIN; LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
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207
82
287
149
88
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9
LEG8_RAT
Q62665;
01-~
                                                                                                                                                                                                 DOMAIN
SEQUENCE
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                                                                                                                                      234 GLYPSKSILLSGTVLPSAQRFHINLCS-GNHIAFHLNPRFDENAVVRNTQIDNSWGSEER 292
                                                                                                                         293 SLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTH 352
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                              .
9
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GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 279;
                                                             32; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                 01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
32 KD BETA-GALACTOSIDE-BINDING LECTIN (32 KD GBP).
CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112; DB 1; Le
Pred. No. 1.12e-03;
12; Mismatches 13;
P -> L (IN REF. 1).
E -> G (IN REF. 1).
ZEOD41C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 125; DB 1;
Pred. No. 9.88e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D6BA48DB CRC32;
                                                                                                                                                                                                                                279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P11116; 1SLT.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 2.
GALAPTIN; LECTIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                             HIRABAYASHI J., SATOH M., KASAI K.-I.;
J. BIOL. CHEM. 267:15485-15490(1992).
                                                                                                                                                                                                                                                                                                                                                                                                 ARATA Y., HIRABAYASHI J., KASAI K.-I.;
J. BIOL. CHEM. 272:26669-26677(1997).
                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31809 MW;
                    39518 MW;
                                       Match 12.8%;
Local Similarity 25.2%;
es 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.4%;
Best Local Similarity 35.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 202-220.
MEDLINE; 92348337.
270 2
313 3
355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AA;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 92348399.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97476274
                                                                                                                                                                  353 VQT 355
                                                                                                                                                                                      131 VHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 8
LE33_CAEEL
Q09581;
                                                                                                                                                                                                                               LE32_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
SEQUENCE
                    SEQUENCE
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P1
PROSITE;
 CONFLICT
           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                    Best Loca
Matches
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AC Q0
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-!- DEVELOPMENTAL STACE: VERY LOW LEVELS IN WHOLE EMBRYOS, HIGH LEVELS IN ADDLT TISSUES.
-!- SIMILARITY: BELOWS TO THE GALAPTIN (S-LECTIN) FAMILY.
EMBL; U09824; G717032.
-- PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
GALAPTIN; LECTIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HLSLPFEARLNASMGPGRTVVVKGEVNTNATSFNVDLVAGRSRDIALHLNPRLNVKAFVR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAINS.
-!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, CARDIAC MUSCLE,
                                                                                                                                                             EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
MEDLINE; 95155445.
HADARI Y. K., PAZ K., DEKEL R., MESTROVIC T., ACCILI D., ZICK Y.;
J. BIOL. CHEM. 270:3447-3453(1995).
-i- FUNCTION: POSSESS SUGAR BINDING AND HEMAGGLUTINATION ACTIVITY.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGALS8.
RATUUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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185 316 GALAPUIN 2.
248 254 BETA-CALACTOCIDE (BY SIMILARITY).
316 AA: 36038 MW; 96341BC7 CRC32;
01-OCT-1996 (REL. 34, CREATED)
1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDVATION UPDATE)
PROBABLE 33 KD BETA-GALACTOSIDE-BINDING LECTIN (33 KD GBP).
                                                                                                                                                                                                                                                                                                            -: FONCTION: BINDS GALACTOSE (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
EMBL; ZR892: 32606; -:
WORMPEP: XR892: CEOTIN GALACTOSIDE; 1.
PROSTIE: FS00309: LECTIN GALACTOSIDE; 1.
DOMAIN 142 289 GALAPTIN 1.
DOMAIN 142 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 112; DB 1; Length 289;
Pred. No. 1.12e-03;
17; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                         SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::| |::||| ::||| :::|
5 LEVPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSLRDQAA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 AA; 32991 MW; 3329858D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECIIN-8 (30 KD S-TYPE LECTIN) (RL-30).
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llarity 22.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 11.4%;
Similarity 29.3%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                 CAENORHABDITIS ELEGANS
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Best Local Similarity 2
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2; LLOYD C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
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P07583;
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-!- SUBUNTT: MONOMER.
-!- ILSSUE SPECIFICITY: HIGHLY EXPRESSED IN FULL-LENGTH FORM IN SMALL
AND LARGE INTESTINE AND STOMACH BUT WAS NOT DETECTED IN OTHER
TISSUES INCLUDING LUNG, LIVER, KIDNEY, AND SPLEEN.
-!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                           241 NSFLQDAWGEEERNITCFPFSSGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKD-LSSI 299
                                                                             | : ||: ||: :||:: :||:: :||:: | : :||:: | : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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01-CCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
15-UTL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ASAGNONES, S.H., LEFFLER H.,
J. BLOL. CHEM. 268:5929-5939(1993).
-!- FUNCTION: GALECTIN THAT BINDS LACTOSE AND A RELATED RANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LEST ANNOTATION UPDATE)
UDP-N-ACETIZGLUCOSAMINE--DOLICHYL-PHOSPHATE N-
ACETILGLUCOSAMINE-POLICHYL-PHOSPHATE N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RATTUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKER.
GALAPTIN 2.
BETA GALACTOSIDE (BY SIMILARITY).
9870240B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                               324 AA
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PROSITE; PS00309; LECTIN GALACTOSIDE; 2.
GALAPTIN; LECTIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALAPTIN 1.
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Similarity 23.7%;
31; Conservative
                                                                                                                                                                              DTLAVDGDIRLLDVRS 315
                                                                                                                                                                                                                            | : | ::| |:|
118 RELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M73553; G294572; -.
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257 2
324 AA;
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GPT_YEAST
P07286;
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P38552;
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ALJINOVIC G., POHL F.M., POHL T.M.;
SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CATALYSES THE INITIAL STEP IN THE SYNTHESIS OF DOLICHOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALLUS GALLUS (CHICKEN).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, AVES, NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 GLEVGQCIVLAILALLNDLLYFSMGPLATRDSHRFSAVLIIPFLGVSLALWKWNRWPATV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 86130505.
OHYAMA Y., HIRABAYASHI J., ODA Y., OHNO S., KAWASAKI H., SUZUKI K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: GLYCOSYLATION.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                 P-P-OLIGOSACCHARIDES.
-!- CATALYTIC TOPP-N-ACETYL-D-GLUCOSAMINE + DOLICHYL
- PHOSPHATE = UMP + N-ACETYL-D-GLUCOSAMINKL-DIPHOSPHODOLICHOL.
-!- ENZYME REGULATION: INHIBITED BY TUNICAMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSYLTRANSFERASE; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOLICHOL RECOGNITION (POTENTIAL)
EFC9A131 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: SIGNIFICANT, TO OTHER SPECIES GIPT.
-!- SIMILARITY: SOME TO YEAST ALG1, DPM1, AND SEC19 AND TO EMBL; YOUL26; 446485; -.
EMBL; Z301126; 4536553; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 1; Length 448;
Pred. No. 9.03e-03;
21; Mismatches 32; Indels
(N-ACETYLGLUCOSAMINE-1-PHOSPHATE TRANSFERASE) (GLCNAC-1-P
TRANSFERASE) (TUNICAMYCIN RESISTANCE PROTEIN 1).
ALG7 OR TUR1 OR YEB143C OR YEB1628.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
BETA-GALACTOSIDE-BINDING LECTIN (14 KD LECTIN) (C-14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                   MEDLINE; 87203393.
HARTOG K.O., BISHOP B.;
NUCLEIC ACIDS RES. 15:3627-3627(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50368 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%;
ilarity 24.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 FVGDTYCYFAGMVFAVV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 LISAPFLFYPORFFEVL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
276
303
329
407
439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A27522; A27522
SGD; L0000078; ALG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 AA;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RETICULUM.
                                                                                                                                                                                                                                                                                           STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFERASE;
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-!- SUBCELLOLAR LOCATION: OUTER MEMBRANE.
-!- SIBALARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
EMBL; M9803; G151435; --
PROSITE; PS00430; TONB-DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01456; TONB_DEPENDENT_REC_2; 1.
OUTER MEMBRANE; IRON TRANSPORT; TRANSPORT; TONB BOX; SIGNAL; RECEPTOR.
SIGNAL
25 POTENTIAL.
26 746 FERRIC ENTEROBACTIN RECEPTOR.
                                                                              Gaps
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEUDOMONAS AERUGINOSA.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
PSEUDOMONADACEAE.
                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 DVPSAHAIREQLRAGSEIHVRGHVTHKHKDFSVELLS-GPHI-V-LHVNF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEAN C.R., POOLE K.;
J. BACTERIOL. 175:317-324(1993).
-!- FUNCTION: SPECIFIC RECEPTOR FOR THE SIDEROPHORE FERRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 97; DB 1; Length 184; 7.3%; Pred. No. 1.80e-01; tive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.30e-01;
15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 21.0 KD PROTEIN R07B1.10 IN CHROMOSOME X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 138 GALAPTIN.
184 AA; 20991 MW; EAF0FA73 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFEA_PSEAE STANDARD; PRT; 746 AA. 005098; 01-JUN-1994 (REL. 29, CREATED) 01-WV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) FERRIC ENTEROBACTIN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALAPTIN.
                                                                                                                                                                                                                                                                                                                                                 PRT;
Best Local Similarity 33.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 37.3%;
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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MEDLINE; 93123148.
                                                                                                                                                                                    238 QRW 240
                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                              YRNA_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                        64 SRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                         009610;
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Matches
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RESOURCE FROM N.A.

RESOURCE FROM N.A.

RESTRAIN-ATCC 14405 / ZOBELL;

RA ZUMET W.G., VIEBROCK-SAMBALE A., BRAUN C.;

RL GUR. J. BIOCHEM. 192:591(1990).

CC -!- SUBCLELULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).

CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).

CC -!- SIGHEL, X53676; G45849; J.

DR PIR, S1384; S13584.

DR PIR, S1384; S13584.

DR PROSITE; PS00211, ABC_TRANSPORTER; 1.

DR PROSITE; PS00211, ABC_TRANSPORTER; 1.

TRANSPORT; ATP-BINDING; COPPER; MEMBRANE.

NP BIND 36 43 ATP (POTENTIAL).

NP BIND 36 43 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                HERBAYASHI J., KAWASAKI H., SUZUKI K., KASAI K.-I.;
J. BIOCHEM. 101:775-783(1987).
-!- FONCTION: THIS PROTEIN BINDS BETA-GALACTOSIDE. ITS PHYSIOLOGICAL
FUNCTION IS NOT YET KNOWN. IT MAY BE INVOLVED IN THE REGULATION OF
DIFFERENTIATION.
-!- SUBBUILT: MAINLY IN THE INTESTINE (ADULT), MAINLY IN
THE SKIN (EMBRYO).
-!- SHILLARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSEUDOMONAS STUTZERI (PSEUDOMONAS PERFECTOMARINA).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION.
BETA-GALACTOSIDE (POTENTIAL)
2A62CF00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 10.1%; Score 99; DB 1; Length 134; Local Similarity 27.9%; Pred. No. 9.41e-02; es 12; Conservative 15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GLKPGQRLTVKGIIAPNAKSFVMNLGKDSTHLGLHFNPRFDAH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P11116; 1SLA.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
GALAPIIN; LECTIN; ACETYLATION; MULTIGENE FAMILY.
KASAI K.-I.;
BIOCHEM. BIOPHYS. RES. COMMUN. 134:51-56(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REL. 17, CREATED)
(REL. 17, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDAT
COPPER TRANSPORT ATP-BINDING PROTEIN NOSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M11674; G211807; -...
EMBL; D00311; G222800; -...
EMBL; D00309; G222800; JOINED.
EMBL; D003109; G222800; JOINED.
EMBL; D00310; G222800; JOINED.
PIR; AX0042; LNCH14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 B
14932 MW;
                                                                                                                                 OHYAMA Y., KASAI K.-I.;
J. BIOCHEM. 104:173-177(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 AA;
                                                                           SEQUENCE FROM N.A. MEDLINE; 89033999.
                                                                                                                                                                                                                                     TISSUE-EMBRYO;
MEDLINE; 87250364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEUDOMONADACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOSF_PSEST
P19844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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NIT_MET

RREPRESENTATION OF THE PROPERTY OF THE PROPERT

Best Loc Matches

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RESULT

NOSF

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FT SIMILAR 39 44 TONB BOX.

FT SIMILAR 729 746 TONB C-TERMINAL BOX.

SQ SEQUENCE 746 AA; 80967 MW; 3BC231B9 CRC32;

Ouery Match 9.7%; Score 95; DB 1; Length 746;

Best Local Similarity 37.8%; Pred. No. 3.42e-01;

Matches 14; Conservative 10; Mismatches 12; Indels 1; Gaps 1;
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Search completed: Tue Dec 15 15:55:27 1998 Job time : 16 secs.

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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tue Dec 15 18:30:42 1998; MasPar time 1134.44 Seconds 1365.449 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-109-864-1 (1-865) from US09109864.seq 865 Title: Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Query 0 Dbase 0; .. Nmatch STD

2275026 seqs, 895388244 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Database:

5:9b_est1 6:9b_est10 7:9b_est11 8:9b_est12 9:9b_est13 10:9b_est14 11:9b_est15 12:9b_est16 13:9b_est17 14:9b_est18 15:9b_est18 15:9b_est2 17:9b_est2 17:9b_est2 18:9b_est2 17:9b_est2 19:9b_est2 18:9b_est2 17:9b_est5 22:9b_est6 23:9b_est2 24:9b_est8 25:9b_est9 26:9b_gss1 27:9b_gss2 28:9b_gss3 29:9b_gss4 embl-est55 l:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est107

Mean 12.059; Variance 7.331; scale 1.645

Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No.	2.06e-287	.64e-199	.39e-187	.44e-120	2.17e-53	14e-28	.89e-17	.79e-13	.94e-11	.77e-10	.77e-10	.32e-10	.32e-10
Pre	!	~	٦	Ч	~	•	•	~	4	Н	-	ဖ	ဖ
Description	EST181872 Jurkat T-cel	yo59h05.rl Homo sapien	yo59h05.sl Homo sapie	EST55685 Infant adren	ze63a11.rl Soares reti	ze46b12.rl Soares reti	97SN1787 Rice Immature	97SN1787 Rice Immature	yh96a12.rl Homo sapien	Dictyostelium discoide	qc33f09.x1 Soares_preg	97SN1784 Rice Immature	Dictyostelium discoide
ព	AA311108	H30148	H27468	AA349100	AA020729	AA001029	AA754459	AA754459	R37188	C84867	AI128239	AA754458	C24325
80	24	16	19	25	22	22	12	12	'n	12	11	12	7
S Ouery Match Length DB	496	411	422	227	099	434	252	252	448	341	492	247	558
Query Match	53.5	38.8	36.9	25.5	13.9	9.5	7.1	6.4	5.9	5.8	5.8	5.7	5.7
Score	463	336	319	221	120	80	61	52	51	20	20	49	49
Result No.	П	7	m	4	Ŋ	9	7	ω	σ	10	11	12	13
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Other_ESTs: THC124424 Contact: Kerlavage, AR Bloinformatics The Institute for Genomic Research

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    Tel: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Site_1: EcoRI; Site_2:
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Pred. No. 2.06e-287;
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                                                                                                  /organism="Homo sapiens"
/note="Vector: pBluescript SK-;
XhoI"
                                                                                                                                       /db_xref="ATCC (inhost):157086"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells V"
Rockville,
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<1. .>496
113 c 151 g 103
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Medical Center Drive,
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larity 99.2%;
Conservative
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Best Local Similarity
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of modified pTyT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soare and M.Fatima Bonaldo.
                                                                                                                              Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcoptersygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 411)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tan, F., Tanses, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Washu Merck EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 264
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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yo59h05.sl Homo sapiens cDNA clone 182265 3'
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Pred. No. 2.64e-199;
0; Mismatches 13;
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/clone="182265"
113 c 121 q 79
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Best Local Similarity 95.7%;
Matches 360; Conservative
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                                                                                                                                                                                                                     REFERENCE
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/organism="Homo sapiens"
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Location/Qualifiers
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Contact: Kerlavage, AR
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llarity 98.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
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Best Local Similarity
Matches 223; Conserv
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                                     Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcoptraygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 422)
1 (bases 1 to 422)
1 (bases 1, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hullman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fight quality sequence stops: 309
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Unpublished (1995)
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108 c 12
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Best Local Similarity 91.7%;
Matches 386; Conservative
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H27468
9897458
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JOURNAL
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 ACCESSION
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Mams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

S. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Rirkness, E.F., Weinstock, K.G., Goocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man'Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.E., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hann, M.C., Hedblom, E., Hikle, P.S.J.T.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.L., Saudek, D.M., Shirley, R.,

Small, R.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao', L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dinke, D., Fenris, A., Fischer, C., Hastings, G.A.,

Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Metsner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                     AA349100 227 bp mRNA EST 21-APR-1997 EST55685 Infant adrenal gland II Homo sapiens cDNA 5' end, mRNA
/note="Organ: adrenal gland; Vector: pBluescript SK-;
Site_1: ECOR1; Site_2: XhoI"
/db_xref="AACC (inhost):150218"
/db_xref="texon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Pred. No. 1.44e-120;
0; Mismatches 4;
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human,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2180 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 444.
Location/Qualifiers
1. 660
                                                             61 ACAIGCICITCCCCAGGGICICICGCCTGGGCAGGICATCAIAGIACGGGGACIGGICII 120
                                                                                                  GCAAGAGCCGAAGCATTTTACTGTAAGCCTGAGGGACCAGGCTNCCCATGCTCCTGTAAC 180
                                                                                                                9
            Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 660)
Heiliter, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wasterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
1 AGAGTACCCAGGTGGACATCCTTTCCTGCTGATGAGCCCCAGGCTGGAGGTGCCCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fex: 314 286 1810
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zavilu29 434 bp mRNA EST 29-NOV-1996 ze46bl2.rl Soares retina N2b4HR Homo sapiens cDNA clone 362015 5/ similar to contains Alu repetitive element; contains L1.tl L1 AA001029 g1437096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashUnwarck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2264 Std Error: 0.00
Seq primer: mob.REGA+ET
                                                                                                                               331 ctgaagctggcgctcaatgggcagggctgggggccaccagcatgaaccagcaggcctg 390
                                                                                                                                                                                                   60 GAGCAGCTGCGNGA-CTCCGGATCAGTGGAAGTGTCCAGCTCTACTGTGTCCACTCCTGA 118
                                                                                       1 CTGAAGCTGGCGCTCAATGGGCAGGGGCTGGGGGC-ACCAGCATGAACCAGCAGGCCCTG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 434)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hellman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                               Gaps
                                               5
  Length 660;
                                               Indels
Score 120; DB 22; L
Pred. No. 2.17e-53;
0; Mismatches 1;
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/clone_lib="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
                                                                                                                                                                                                                                                               High quality sequence stop: 345.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson, R.
The WashU-Merck EST Project
  Query Match 13.9%;
Best Local Similarity 96.2%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
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Query Match
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AUTHORS
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/organism="Oryza sativa"
/organism="Oryza sativa"
/organism="Oryza sativa"
/cultivar="Metor: Baluescript SK(+); Site_1: EcoRI; Site_2:
/hote: "Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDNA library inserted into lambda ZARII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db.ref="taxon:4530"
/clone="97SN1787"
/clone="97SN1787"
/clone="97SN1787"
/clone="15" Rice Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                     AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
4A754459
92801165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 252)

Nahm, B.H., Kim, M.Y., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.

Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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                                                                                                                                                                                                        72 NVSGDWHYWBVBNTKVDVGNHTRC-SRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYB 130
                                                                                                                                                                                   1 ACCAGCAGGCCCTGGAGCAGCTGCGNGA-CTCCGGATCAGTGGAAGINTCCAGCTCTACT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 CCCBAWMITSYBCHGNBVWVCVASHGNYMSVHN-CIBRGIHCDCKNVNWSTMTWGTVNWB 71
                                                                                                                                                   Gaps
                                                                                                                                                   4;
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                                                                                                                                                                                                                                                                           Length 434;
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                                                         4 others
                                                                                                          Score 80; DB 22; Length 434 Pred. No. 4.14e-28; 0; Mismatches 2; Indels
                     resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Fel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.1%; Score 61; DB 12; Ler
Best Local Similarity 14.3%; Pred. No. 9.89e-17;
Matches 32; Conservative 110; Mismatches 79;
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin
                                                     94 t
                                                       б
                                                     104
                                                                                                          Query Match 9.2%;
Best Local Similarity 94.5%;
Matches 104; Conservative
                                    .>434
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AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence. AA754459 92801165
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="975N1787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="fmmature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
12 coli 9 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, M.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
594 gagetttg-ggeetgaaggaaggeacaagagtgeaaaggtteetegaaactetgeacette 652
                                                                                                                        653 ctccaccaggagcctgggatatggctccatctgccttcagggcctggactgcactcacag 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 DVKSSTNTWGV-TBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCVRKYCVMMMTKKVV 219
                                                                                       BIGCMICIMWCWBHYNIKCIASGWHISINYDVKSSINIWGVIBSYDKSMHGYWCSBBVKY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 MSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRB 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 VTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNTKCTASGWHTSTNY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 ctgtgagtgcagtccaggccctgaaggcagatggagccatatcccaggctcctggtggag
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                                                                                                                                                                                                                                     191 HTKVSTTRATRSYTCVRKYCVMWMTKKVVKKYHVVBBGCHBTDS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tech, RDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Cytogenetics
National Inst. of Agri. Sci. and
Wuwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poales; Poaceae; Oryza.
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Local Similarity 10.0%;
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ACCESSION KEYWORDS ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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AI128239 492 bp mRNA EST 11-SEP-1998
G233169.x1 Soares_pregnant_uterus_NDHPU Homo sapiens cDNA clone
IMAGE:1711433 3' similar to gb: M68220 CELL DIVISION PROTEIN KINASE
2 (HUMAN); contains element MSR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Organism="Homo sapiens"

/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI: 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
AACTGGAAGAATTCGCGCCCCCTTTTTTTTTTTTTT 3']
AACTGGAAGAATTCGCGCCCCTTTTTTTTTTTTTT 3']
(Pharmacia), digested with Not I and cloned into the Not
and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 492) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1150
Email: Robert_Strausberg@inih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd.ET from Amersham
High quality: sequence stop: 420.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (O7-JAN-1998) to the DDBJ/EMBL/GenBank databases.
Submitted (O7-JAN-1998) to the DDBJ/EMBL/GenBank databases.
Sciences: 1-1-1 Ten-noudai, Tsukuba.shi 305-0006, Japan (E-mall:qxurushi@bank.dna.affrc.go.jp, Tel:+81-0298-53-4664, Pax:+81-0298-53-6614)
PROJECT - 'Dictyostelium discoideum cDNA project in Japan', Location/Qualifiers
                                        Mizuno,H., Morio,T. and Tanaka,Y.
Developmental cDNA in Dictyostelium discoideum (229)
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 341;
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Pred. No. 1.77e-10;
0; Mismatches 21;
  Eukaryotae; Dictyosteliida; Dictyostelium.
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                                                                                                                                                                                                                                                                                                                                                      /strain="AX4"
/db_xref="taxon:44689"
/clone_lib="SS"
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29 c 35 c
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Best Local Similarity 77.2%;
Matches 71; Conservative
                                                                                                   2 (bases 1 to 341)
Urushihara, H.
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Unpublished (1997)
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1 (bases 1 to 448)
Hillier,L., Clark, N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Dictyostellum discoideum (strain:AX4) slug cDNA to mRNA, clone_lib:SS.
Dictyostellum discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Dictyostelium discoideum slug CDNA, clone SSG869,
C84867
                                                                                       yh96a12.rl Homo sapiens cDNA clone 137566 5'.
837188
9794644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
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                       592 tgtagactcagtctcgtgaccccagaggtg 563
220 KKYHVVBBGCHBTDSKCKTMWMTNKHVMTS 249
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86 c 9
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Best Local Similarity 91.8%;
Matches 56; Conservative
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9 VWRGCCCCBAWMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBW
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/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: Paluescript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional cDNA library inserted into lambda ZAPII
vector at 5; end with EcoRI and 3; end with XhO I site."
/db_xref="taxon:4530"
/clone="97SN1784"
/clone="197SN1784"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duza sativa

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Embryophyta: Trachosphyta; seed plants; Magnoliophyta; Liliopsida;

Poales; Poaceae; Oryza.

1 (bases 1 to 247)

Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,

Kim,M.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,

Lee,M.C. and Eun,M.Y.

Lee,M.C. and Enn,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA754458 247 bp mRNA EST 20-JAN-1998
SYSNTR4 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SN1784, mRNA sequence.
AA754458
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 92 bhail: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
went through one round of normalization. Library constructed by M. Fatima Bonaldo."

Adb_xref="laxon:9606"
/clone="IMAGE:1711433"
/clone=lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
/dev_stage="adult"
/lab_host="bHI08"
198 c 89 g 131 t
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Pred. No. 6.32e-10;
114; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                             Score 50; DB 17; Le
Pred. No. 1.77e-10;
0; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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larity 77.2%;
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Best Local Similarity 11.6%;
Matches 27; Conservative
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Matches 71; Conser
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C24325 558 bp mRNA EST 09-JUN-1997
Dictyostelium discoideum gamete cDNA, clone FC-AQ23, mRNA sequence.
C24325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-MAY-1997) to the DDBJ/EMBL/GenBank databases. Hideko Urushihara, University of Tsukuba, Institute of Biological Sciences; Ten-noudal 1-1-1, Tsukuba-shi, Ibaraki-ken 305, Japan (E-mail:d402hu8sakura.cc.tsukuba.ac.jp, Tel:0298-53-4664, Fax:0298-53-6614)
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mRNA sequence.
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gagctccggatcagtggaagtgtccagctccactcctgaaggatggttcca 462
                                                                                      69 YYARSKYGYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWB-TAYCDYBH 127
                                                                                                                                        521
                                                                                                                                                                                128 YBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRY-TGYDKTDSDCGGGCWRKVTYGSSB 186
                                                                                                                                                                                                                         522 ttaaaccatccacctgaacaccagcacatcagggcctggttcacctctgggggtcacgaga 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92190079
EST; EST(expressed sequence tag).
Dictyostelium discoideum (strain:RAX3) Sexually mature Gamete
68
                                                                                                                     |: : :| ::::| :| :| :| ... | 463 ggaaataccgcagaaaaaaaaaagag-tcagccactccccccag
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EST: EST(expressed sequence tag).
Dictyostelium discoideum (strain:AX4) slug cDNA to mRNA,
clone_lib:SS.
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                                                                                                                                                                                                                                                                                                        187 YBRCG-VNVMVRTTSMWTDKSTKMBSMDMSRRSRVHYGRWMBNKKRGMSRNW 237
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Dictyostelium discoideum
Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
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Dictyostelium discoideum slug cDNA, clone SSJ350,
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Pred. No. 6.32e-10;
0; Mismatches 6
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Sazuki,K., Shimizu,H. and Urushiihara,H.
Sexual cDNA in D. discoldeum
Unpublished (1997)
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67 c 94 g 172 t
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/db_xref="taxon:44689"
/cell_type="Gamete"
/clone_lib="FC"
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Best Local Similarity 90.2%;
Matches 55; Conservative
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Urushihara, H.
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Direct Submission Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases. Hideko
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                                                                                                                                         Direct Submission
Submitted (17-MAR-1998) to the DDBJ/EMBL/GenBank databases.
Motonobu Yoshida, Kinki University, Research Institute of Food
Science, Nakamachi 3377, Nara 631, Japan
(E-mail:yoshida@ew266.nara.kindai.ac.jp,
Tel:+81-742-43-1511(ex.3005), Fax:+81-742-43-1155)
PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urushihara, University of Tsukuba, Institute of Biological Sciences; 1-1-1 Ten-noudai, Tsukuba-shi 305-8572, Japan (E-mail:qxurushi@bank.dna.affrc.go.jp, Tel:+81-0298-53-4664, PROJECT - 'Dictyostelium discoideum cDNA project in Japan'. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST; EST(expressed sequence tag).
Dictyostellum discoideum (strain: AX4) slug cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                   2 others
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Pred. No. 2.23e-09;
0; Mismatches 20; Indels
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Eukaryota; Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostelium.
I (bases 1 to 241)
Urushihara,H.
Developmental cDNA in Dictyostelium discoideum
Published Only in DataBase (1998) In press
Urushihara,H.
                                                                    Developmental cDNA in Dictyostellum discoideum Published Only in DataBase (1998) In press (bases 1 to 151)
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/organism="Dictyostelium discoideum"
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/organism="Dictyostelium discoideum"
Dictyostellum discoideum
Wararyota; Dictyostellida; Dictyostellum.
1 (sites)
Yoshida,M.
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                                                                                                                                                                                                                                                                                                                     /strain="AX4"
/db_xref="taxon:44689"
/clone_lib="ss"
/dev_stage="slug"
a 1 c 5 g 4
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Best Local Similarity 77.3%;
Matches 68; Conservative
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Best Local Similarity 90.0%;
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Search completed: Tue Dec 15 18:57:34 1998 Job time : 1612 secs.

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7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4.w.w.w.		AF012089 AF026266 ATPYK10 MMU80780 BTU73585	Drosopnia melanogaste Iucilia cuprina cuticl A.thaliana mRNA for th Mus musculus putative Bos taurus Fanconi ane	melanogaste prina cuticl mRNA for th us putative Fanconi ane		

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AF012089 HCU45456 HCU4545B BFNRSUB HAY12278 DMU41222 RNU76551 AF032396 DDU448271 A52184 A52184	PFSC04009 PFSC04059 PFMAC10550 AC005506 HAX12282 DDILI3A CEMCEIA 166494 122446 122446 122446 122446 122446 122446 122446 12246 122446	ALIGNMENT by DNA 11 Cosmid cs cs cs cs dia; Eutheri	14) (Y.P., Brignac, S. J., Davis, C., E. Davis, C., E. Davis, C., I. Davis, Gordor, H.R., Gordor, T., Hinson, S., N., Oliver, T., R., Oliver, T., R., Chult, R., Schult, R.	Br tvi č., iso Liv	
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DB 26; Length 35414;

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Glorda, W., Ohmachi, T., Shaw, D.R. and Ennis, H.L.
A shared internal threonine-glutamic acid-threonine-proline repeat
defines a family of Dictyostellum discoideum spore germination
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Direct Submission
Submitted (17-APR-1990) Herbert L. Ennis, Roche Institute of
Molecular Biology, 340 Kingsland Street, Nutley, NJ 07110-1150,
3 (bases 1 to 1098)
                                                                                                                                                                                                                                                                                                                                tgtgagtgcagtccaggccctgaaggcagatggagccatatcccaggctcctggtggagg 652
                                                                                                                                                                                                                                                                               651 aaggtgcagagttcgaggaacctttgcactcttgtgccttccctcaggcccaaagctcct 592
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Dictyosteliu discoideum cellulose binding protein (CelB) gene,
                  Gaps
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Location/Qualifiers
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Dictyostellum discondeum
Eukaryotae; mitochondrial eukaryotes; Dictyostellida;
Dictyostellum.
                  Indels

    2982
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/strain="AX-3"

Pred. No. 2.20e-137;
0; Mismatches 4;
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Biochemistry 29 (31), 7264-7269 (1990)
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Best Local Similarity 97.9%;
Matches 523; Conservative
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                                                                                                                              /note="spore germination-specific protein; formerly called 270-11"
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NDNSLIYHTWELVYDOTSLTLPTYRKAGPINPEETIIFGYISRNSTDYTFALSPTCSD

SSPPPPPETPTETPTETPTETPTFTPTETPTETPTETPTFTFTPTFTFTPTFTSDYTFALSPTCSD

SEIPPPPETDTPTPTSSSSSSSSSSSSSTOPPITPPPTTGTSCLAQVQQXVINSW

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GSHTFGYIVKSAELSDLEGVQYTC"

1254. .1340

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/gene="Celb"
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VVSSGGQIPITTTSSTTTDGSSTPSTPTSTTSASTTTSGGSATTTTGEPITDGSNGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSEPMG50 1927 bp RNA PRI 30-JUN-1993
H.sapiens mRNA for 50 kDa erythrocyte plasma membrane glycoprotein.
X64594 S46252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-MAR-1992) K. Ridgwell, University of Bristol, Dept o Biochemistry, School of Medical Sciences, University Walk, Bristol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolation of cDNA clones for a 50 kDa glycoprotein of the human erythrocyte membrane associated with Rh (rhesus) blood-group
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1927)
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Pred. No. 3.81e-04;
0; Mismatches 19; Indels
          /tissue_type="germinating spore" 984. .1253
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Biochem. J. 287 (Pt 1), 223-228
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                                             /gene="CelB"
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larity 79.3%;
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SOGOKRNIGIKMMINADFSAATVLISFGAVLGKTSPTQMLIMTLETYFFAHBEYLVS
BIFKASDIGASMTIHAFGAYFGLAVGATLYRSGLRKGHEDESSAYSDLFAMIGTLFV
WMFWPGFNSA LAEPGKQCRAIVDTYFSLAACVLTARAFSSLVEHRGKLNWHIQNAT
LAGGVAVGTCADMAIHPFGSMIIGSIAGMVSVLGYKFLTPLFTTKRHBTGCYHNLH
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                                                                                                                                                                                                     /codon_start=1
/product="15.0 kDa erythrocyte plasma membrane glycoprotein"
/db_xref="PID:31195"
/db_xref="SWISS-PROT:Q02094"
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Fidock,D.A.
Direct Submission
Submitsed (16-SEP-1993) David A. Fidock, Laboratory of bio-medical parasitology, Pasteur, Institute, 25, rue du Dr. Roux, Paris,
PARIS, 75724 CEDEX 15, France
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Plasmodium falciparum
Eukaryotes; Alveolata; Apicomplexa;
Bacaryotae, mitochondrial eukaryotes; Alveolata; Apicomplexa;
Bacmosporida; Plasmodium.
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/clone="DG21"
/dev_stage="Sporozoite, liver stage, erythrocytic ring
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/standard_name="glycosylation site"
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                             /tissue_type="bone marrow, liver" /chromosome="6"
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1. 2787
/organism="Plasmodium falciparum"
/strain="T9/96"
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P.falciparum gene for STARP antigen.
226314
/dev_stage="foetal"
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*** SEQUENCING IN PROGRESS *** Plasmodium falciparum 3D7 chromosome
12 PFYAC492 genomic sequence; HTGS phase 1, 36 unordered pieces.
AC005308
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/translation="MIHIFYKTAIFTLSIWTTLLYSNKNLKCNFYNNNNLSTYVIKH
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* arbitrary. In some cases, the exact lengths of the gaps

* between the contigs are also unknown; these gaps are presented

* as runs of N as a convenience only. When sequencing is complete,

* the sequence data presented in this record will be replaced

*by a single finished sequence with the same accession number.
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
Submitted (21-JUL-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 244649)
Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
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On Aug 20, 1998 this sequence version replaced gi:3334987
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Pred. No. 1.50e-02;
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/cell_line="T9/96 blood stage culture"
                                                                join(1. .806, 982. .2787)
/product="STARP antigen"
join(735. .806, 982. .2724)
                                                                                                                        'product="STARP antigen"
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malaria parasite P. falciparum.
Plasmodium falciparum
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                           /chromosome="8"
1. .806
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/number=1
982. .2787
/number=2
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68; Conservative
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Matches 68; Conser
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                                                                                                                                Unclassified
1 (bases 1 to 144)
Jacobs, K., McCoy, J.M., LaVallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M. and Spaulding, V.
Secreted proteins and polynucleotides encoding them
Patent: US 5723315-A 26 03-MAR-1998;
Location/Qualifiers
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Mahoney,W.C.
PRODUCTION OF MATURE PROTEINS IN TRANSFORMED YEAST
Patent: WO 8401173-A 1 29-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                              4 others
                                    120 others
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Pred. No. 2.74e-02;
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Pred. No. 2.74e-02;
0; Mismatches 5;
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Pred. No. 1.50e-02;
0; Mismatches 20;
/organism="Plasmodium falciparum"/db_xref="taxon:5833"
/chromosome="12"
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                        /chromosome="12"
25158 c 27624 g 92761
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Sequence 1 from Patent WO 8401173.
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142 c 158 g
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Best Local Similarity 91.2%;
Matches 52; Conservative
                                                                      Query Match 5.5%;
Best Local Similarity 77.3%;
Matches 68; Conservative
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Best Local Similarity 87.7%;
Matches 50; Conservative
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AFU12089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089
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1274. .2071
/note-"extreme transcription initiation at -535 relative
to the AUG translation start codon; promoter element
between positions -694 and +103 relative to transcription
initiation"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 4546 to 4553)
DDICAR 2606 bp DNA PLN 14-JUN-1994
Dictyostelium discoideum cAMP receptor (CAR1) gene, 5' flank
L09637
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Louis, J.M., Saxe, C.L. III. and Kimmel, A.R.
Two transmembrane signaling mechanisms control expression
CMP receptor gene CAR1 during Dictyostellum development
Proc. Natl. Acad. Sci. U.S.A. 90 (13), 5969-5973 (1993)
93317605
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Eukaryotae; mitochondrial eukaryotes; Dictyosteliida;
Dictyostelium.
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                                                                                                                                        Dictyostelium discoideum (strain Ax-3) DNA.
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Pred. No. 2.74e-02;
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1. .1294
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/note="late mRNA"
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Best Local Similarity 88.5%;
Matches 54; Conservative
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Query Match 5.3%;
Best Local Similarity 74.0%;
Matches 71; Conservative
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Best Local Similarity 19.0%;
Matches 28; Conservative
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HFRKSGVLVSLSEQNLVDCSTRYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
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/db_xref="PiD:92305222"
/db_xref="PiD:92305222"
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/db_xref="PiD:92305222"
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SSWYKPNSPATRRAYKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYPFFTQPSGMELEI
YRDNWLEVLGGGIMRHEILQRSGVHQSIGYAFGVGIERLAMVLFDIPDIRLEWRNDS
GFLSQFSEKDLHNLFRYRPFSHTYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLYRSVAG
DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIRSASVDSFNVQ
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/db_xref="PID:92305221"
/translation="MRTAVLLPLLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET
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ASSYPLV"
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Gray,Y.H., Tanaka,M.M. and Sved,J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                     Melaucyucard
Unpublished
3 (bases 1 to 10772)
Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
Direct Submission
Submitted (30-JUW-1997) School of Biological Sciences, University
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location,Qualifiers
                                                                                                                                                                                Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .10772
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_tref="taxon:7227"
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
/note="insertion site of P{CaSpeR}(50C)"
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oin(8110. .9300,9370. .>9532)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"cysteine protease"
872. 7707
/gene="CP1"
8872. 1000
/gene="CP1"
                                                                                   Genetics 144 (4), 1601-1610 (1996)
97132596
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6751. 777.
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/gene="CP1"
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/gene="CP1"
2310. .2426
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/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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/product-"cuticle 12 homolog"

"da_xxref="piD:q2565394"

/translation="KRIIVPRALENVALAAPRPEDATVLRSESEVGPESFOYSYATS-
DGVEAEAQQQLKNVGTDEEAIVVKGSFSFVADDGQTYTVNYVADENGFQPQGAHLPVA
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Saula. E. and Jarmey, J.M.
Direct Submission
Submitted (22-SEP-1997) Tropical Agriculture, Commonwealth
Scientific and Industrial Research Organisation, 120 Meiers Road,
Indoorcopilly, QLD 4068, Australia
Location/Qualifiers
                                                                                                                             1694 WWYWAWTTTMWKWMWTTWKWAMMKTYRTWWWWKMYWTSRTTTTSAMWMWYTWSTWTKYWW 1753
                                                                                                                                                                                                     1754 AYAWMKMWWTRTWARMAWASWARWKWKTSAAAAYSAWRKMWKWWAYRAMKKTWMWAAWKW 1813
                                                                                                                                                   803 accacaaataaataaataataataaatgaccacattctttaagccattgtattttg 744
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Pterygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Calliphoridae, Lucilla.
                                                                                                                                                                                                                                                                                                                                                        AFUZ6266 460 bp mRNA INV 28-OCT-1997
Lucilia cuprina cuticle 12 homolog (cut12) mRNA, complete cds.
AF026266
g2565393
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                                                     Length 10772;
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158 others
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Pred. No. 4.97e-02;
0; Mismatches 25; Indels
                                                                                          Indels
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A.thaliana mRNA for thioglucoside glucohydrolase.
X8941051
                                                     Score 47; DB 18; Le
Pred. No. 2.74e-02;
69; Mismatches 50;
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    460
    /organism="Lucilia cuprina"
/db_xref="taxon:7375"
    460

3046
                                                                                                                                                                                                                                                                             1814 RWKAAWWTWRWYMTTTAAMRAAGCTT 1840
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32. 349
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/codon_start=1
                                                     5.4%;
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gene="HD1"
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Best Local Similarity 91.1%;
Matches 51; Conservative
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   Unpublished
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/translation="MVLQKLPLIGLLLLTIVASPANADGPVCPPSNKLSRASFPEGF
LFGTATAAYQVEGAINETCRGPALMDIYCRRYPERCNNDNGDVAVDFFHRYKEDIQLM
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PGRCSSYVNAKCQDGRSGYEAYLVTHNLLISHAEAVEAYRKCEKCKGGKIGIAHSPAW
FEAHDLADSQDGASIDRALDFILGWHLDTTTFGDYPQIMKDIVGHRLPKFTTEQKAKL
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VYSRGFRSLLKYIKDKYANPEIMIMENGYGEELGASDSVAVGTADHNRKYYLQRHLLS
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Mus musculus putative histone deacetylase (HD1) mRNA, partial cds.
U80780
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Johnson, C.A.
                                                                     Charophyta/Embryophyta group; Embryophyta; Magnollophyta; Magnollopsids; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1741)
Schmidt, K.P., Burrows, P.R., Davies, K.G., Kammerloher, W., Schaeffner, A.R., Buck, F., Cai, D. and Grundler, F.M.W.

A root specific myrosinase in Arabidopsis responding to cyst nematode infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Submitted (04-JUL-1995) K.P. Schmidt, Institut fuer
Phytopathologie, Hermann-Rodewald-Str. 9, D- 24118 Kiel, FRG
Related sequences: A74257 and 234217.
Location/Qualifiers
1. .1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyklo gene; thioglucosidase; thioglucoside glucohydrolase.
Arabidopsis thaliana
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                         /cracinsm="Arabidopsis thaliana"
/strain="Landsberg erecta"
/db_xref="taxon:3702"
/dev_atage="28 days old"
/clsue_type="root tissue"
/clone_lib="pcDM8 COS cell expression library"
/clone="full length in pBsc M13+"
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Pred. No. 4.97e-02;
0; Mismatches 5; Indels (
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/EC_number="3.2.3.1"
/codon_start=1
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1654. .1659
a 332 c 38
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6. .1580
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Schmidt, K.
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Best Local Similarity 91.1%;
Matches 51; Conservative
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Bos taurus
Eukaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotea; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora;
Bovoidae; Bovinae; Bos.
1 (bases 1 to 3795)
1 (bases 1 to 3795)
Cloning of the bovine and Buchwald, M.
Cloning of the bovine and rat Fanconi anemia group C cDNA
Mamm. Genome 8 (7), 522-525 (1997)
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Direct Submission
Submitted (07-067-1996) Genetics, Hospital for Sick Children, 555
University Ave., Toronto, Ontario M5G 1X8, Canada
Location/Qualifiers
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727 .2430
/note="similar to human FAC protein, GenBank Accession
Numbers X66893 and X66894"
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Bos taurus Fanconi anemia group C mRNA, complete cds.
U73585
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/product="Fanconi anemia group C protein"
/db_xref="PID:g2326996"
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Pred. No. 4.97e-02;
0; Mismatches 5;
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/db_xref="taxon:10090"
1. .1999
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/organism="Bos taurus"
/db_xref="taxon:9913"
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ONSRESKLNSWTRILLSH IVSTSRPIKEVGLFNQVLGYAPTDYYPGLLKNMYLSIVS
ELRENHLNGF SGRRCPERVWSLSEDRYPLLTIDPFEPLVEALLYYPGHEPOEVLCPE
FEDAVNRASLLKKISLETSAILCLWIRHLPSLENTWLHILEKLISSERNSLRRIKCPK
KDSLRPEAAACHPAIFRVVDEIFRSALLETDGAPEVLAGLQVFTRCFVEALEKENKQL
KRALKTYPPYASPALVMYLGHPKDIPOGLWHOSIKHISEMLKETVEDHGSYGGPFES
WFLFVHFGGWADITAEQLLABEAGEBREPPAGOQLVRRLLLHFLUMAGGGHTIAR
ECITLMRAPTBAILAMACGHTIAR
EVITLMAQTDAIMNEIIGFLDYTLYRWDHLCVEAHRSRKLARELLEFLRWAGGDVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFUL2089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089
/translation="MAEDSAGLPSNYQFWMQKLSVWTQASTLETQRDICLHLPQFQEF
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Bukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidaa; Drosophilidae; Drosophila.

[ bases 4546 to 4553)

[ cray, Y. H., Tanaka, M. M. and Sved, J. A.

P-element-induced recombination in Drosophila melanogaster: hybrid
element insertion
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Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Gray, Y.H.M. (Sved, J.A.) Preston, C.R. and Engels, W.R.
Direct Submission
Submitted (JOS-JUN-1997) School of Biological Sciences, University
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location, Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                   Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
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Pred. No. 4.97e-02;
0; Mismatches 8; Indels
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/organism="Drosophila melanogaster"
/db_xxef="taxon:7227"
join(872. .1000,2310. .2426,6476. .6/gene="CP1"
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872. .7707
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/gene="CP1"
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/gene="CP1"
/number=1
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/gene="CP1"
2310. .2426
/gene="CP1"
/number=2
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Best Local Similarity 87.1%;
Matches 54; Conservative
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EERFRLKIFNENKHKIAKHNQRFAEGKVSFKLAVNKYADLLHHEFROLMNGFNYTLHK
QLRAADESFKGVTFISPAHVTLPKSVDWRTKGAVTAVKDQGHCGSCWAFSSTGALEGQ
HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
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//translation="MLTLRVOGARHWIKSTRCLASSAAPAKSPSSPPQLEVSGSTVA
//translation="MLTLRVOGARHWIKSTRCLASSAAPAKSPSSPPQLEVSGSTVA
//translation="MLTLRVOGARHWIKSTRCLASSAAPAKSPSSPPQLEVSGSTVA
//translation="MLTLTRVOGARHWIKSTRAWSGSTVANDMN"
PVVTVQQNTPUNLLIPADHVSRQKSDCYTINQQHLLRAHTTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFPRNPGLELFEETWSGTLADPKLILDHP
                                                                                                                                                                                           DSCHFNKGTVGATDRGFTD1PQGDEKKMAEAVATVGPVSVA1DASHESFQFYSEGVYN
EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGF1KMLRNKENQCG1AS
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YFKDWALEVLGGGIMRHEILQRSGVHQSIGYARGVGLERLAMYLEDIPILLFWSNDS
GFLSQFSEKDLHNLFRYRH ISHYPQFTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
DMYBQISLYDKFKHPRGRGKSSVCFRIVYRHMERTLTQARVBHRAVBHRGIASASVDSFNVQ
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Hog cholera virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                         /translation="MRTAVLLPLLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET
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Hog cholera virus strain Riems polyprotein gene, putative NS5
protein region, partial cds.
045456
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.2426,6476. .6690,6751. .7462)
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/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="phenylalanyl tRNA synthetase"
join(8110. .9300,9370. .>9532)
/note="potential orf"
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/product="phenylalanyl tRNA synthetase"
                                                               /product="cysteine proteinase-1"
/db_xref="PID:92305221"
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Pred. No. 4.97e-02;
73; Mismatches 47;
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                                            /codon_start=1
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/gene="CP1"
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Best Local Similarity 17.7%;
Matches 26; Conservative
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6691. .675
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1.472
/organism="Hog cholera virus"
/strain="Riches", C"
/note="vaccine"
/db_xref="taxon:11096"
<1...216
/note="putative NS5 protein coding region"
/codon_start=1
/product="polyprotein"
/db_xref="plb:g1181845"
/translation="NADRIVSKTGNRYIPGEGHTLQGRHYEELVLARKQINNFQGTD
RYNLGPINWAVLRRLRVMMATLIGRGA"
1 (bases i to 472)
Mueller, H.M., Stark, R., Thiel, H.-J. and Pfaff, E.
Comparison of different hog cholera virus strains: Implications for
Viral pathogenicity
Unpublished
2 (bases i to 472)
Mueller, H.M.
Direct Submission
Submitted (11-JAN-1996) Hubert M. Mueller, Federal Research Centre
Submitted, Oli Jan. 1996) Hubert M. Mueller, Federal Research Centre
for Virus Diseases of Animals, Paul-Ehrlich Str. 28, P.O. Box 1149,
Tuebingen, D-72001, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 33; Length 472;
Pred. No. 9.01e-02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.2%;
Best Local Similarity 86.9%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        217. .472
a 85 c
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BASE COUNT
ORIGIN
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AUTHORS
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TITLE
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Search completed: Tue Dec 15 18:30:24 1998 Job time : 1820 secs.

q

Сp

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Tue Dec 15 18:57:53 1998; MasPar time 127.57 Seconds 922.536 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Run on:

not generated. Tabular output

>US-09-109-864-1 (1-865) from US09109864.seq 865 Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 •• Nmatch STD

188442 seqs, 68026449 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq32 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part39 40:part40

Mean 9.274; Variance 8.844; scale 1.049 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length DB	DB	DI	Description	Pred. No
-	47	5.4	992	۳	N40162	Sequence of prepropar	5.38e-07
7	46	5.3	91	σ	051746	Oligonucleotide probe	1.28e-06
m	45	5.2	3437	21	T31478	Spinach debranching e	3.02e-06
4	44	5.1	1066	ω	049943	Human anti-HBs light	7.13e-06
5	44	5.1	8920	11	062924	Carbamoyl-phosphate-s	7.13e-06
9	43	5.0	340	16	099393	Rat allograft inflamm	1.67e-05
7	43	5.0	350	16	09380	Rat allograft inflamm	1.67e-05
∞	43	5.0	1078	4	025785	Protein synthesis inh	1.67e-05
σ	43	5.0	1136	~	N70435	Sequence encoding ins	1.67e-05
10	43	5.0	1364	40	V15228	Heterodimeric human i	1.67e-05
11	43	5.0	1364	56	T48099	Human interleukin-12	1.67e-05
12	43	5.0	1396	4	024371	Natural killer cell s	1.67e-05
13	43	5.0	1558	7	010896	Encodes Xenopus Bone	1.67e-05

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1.67e-05 3.91e-05	.91e-0	.91e-0	.91e-0	.91e-0	.91e-0	.91e-0	.91e-0	.91e-0	.91e-0	.91e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0	.09e-0
Sequence of murine OS 3' fragment of clone	uman HMGI-C aberra	ission	ival	Human survival motor	Human survival motor	Survival motor neuron	Rape acyl-ACP thioest	H	ociated	id pATG29 (A		11075-1 s	Integrin subunit beta	secreted p	Partial cDNA clone en	Human cytoplasmic dom	Alzheimer's disease D	Oil seed rape cystein		ant ac	epti	jinyl	hyalurona		Clone Imd2 encoding i	equence of new	il tung	Human mucosal lymphoc	Ö	ataxia an
Q44391 V00423	ന	\sim	2825	\sim	\sim	10	10	-	m	\sim	m	\sim	T16856	~	05	V04635	T72167	T90173	T90174	N90711	050575	050579	T99541	T61590	005304	N81634	98	0388	Q53403	619
10 38	38	12	22	22	22	22	æ	10	m	21	7	38	18	38	39	39	35	38	38	Н	σ	σ	33	30	Н		33	16	σ	59
3581	Н	S	55	56	æ	58	71	73	0	0	σ	S	œ	ø	ø	^	42	44	47	1569	64	91	11	28	20	85	85	93	10	23
5.4 0.6	٠	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	•	4.7	•	4.7	4.7
43	42		42		42		42	42	42	42	41	41	41	41	41	41	41	41	41		41	41	41	41	41	41			41	41
14 15	16	17	18	19	20	21	22	23	24	52	56	27	78	53	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45
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ALIGNMENTS

RESULT 1 ID N40162 standard; CDNA; 766 BP. AC 16-FEB-1992 (first entry) DE Sequence of preproparathyroid CDNA. KW Processing; Ss. DE Sequence of preproparathyroid CDNA. KW Processing; Ss. Location/Qualifiers FT cds Atag a DN W08401173-A. PN W08401174-A. PN W08401173-A. PN W08401173-A. PN W08401173-A. PN W08401173-A. PN W08401173-A. PN W08401173-A. PN W1. PN W08401173-A. PN W1. PN W

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.T 4
Q49943 standard; cDNA; 1066 BP.
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                   Query Match 5.2%;
Best Local Similarity 88.1%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          33..98
/*tag= b
99..740
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
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30-MAR-1992; JP-074678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUNR ) SUNTORY LTD.
Arima K, Kurihara T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 93-336913/42.
P-PSDB; R42065.
                                                                                                                                                                                                                                                                                                                                                                                            signal_peptide
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9412643-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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TONA encoding a de-branching enzyme - for modifying the branching degree of amylopectin starch synthesised in plants

Claim 1; Page 64-67; 90pp; English.

Statin 1; Page 64-67; 90pp; English.

A partial CDNA clone (T31478) codes for a spinach debranching enzyme (DE) (R98371) useful for modifying the branching degree of amylopectin synthesised in plants. It was obtd. by PCR amplification of CDNA from a spinach leaf CDNA library using probes (T31480-81) based on DE peptides (R98385-86). The clone can be incorporated into a vector from a used for prodn. of recombinant DE, or used in the breeding of transgenic plants; transgenic potatoes showed increased DE activity cand produced a starch having allered viscosity and gel stability properties. Ribozyme or antisense sequences can be used to reduce the DE activity of transgenic plants. The modified starches have food and industrial applies.

Sequence 3437 BP; 1002 A; 676 C; 727 G; 1032 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T31478;
18-SEP-1996 (first entry)
Spinach debranching enzyme cDNA.
Debranching enzyme; R enzyme; spinach; potato; amylopectin; starch;
New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 gggcccactctcctccctcattaaaccatccacctgaacaccaggcaca 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ssvhsyyvvhvvshhhsvhhvvhhvhhvhhvhhvhhvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.3%; Score 46; DB 9; Length 91; 0.0%; Pred. No. 1.28e-06; vative 48; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-1996.
22-DEC-1995; E05091.
22-DEC-1994; DE-447387.
(GENB-) INST GENBIOLOGISCHE FORSCHUNG.
EMMERTMAND M, KOSSMAND J, Renz A, Virgin I;
P-PSDB; R98371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 3
T31478 standard; cDNA to mRNA; 3437 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
201..3095
/*tag= a
                                                                                           BP.
                                                                                                                                                                                                                                                         24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                        JT 2
Q51746 standard; cDNA; 91
                                                                                                                             31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.3%;
Best Local Similarity 0.0%;
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant; ds.
Spinacea oleracea.
                                                                                                                                                                                                                          EP-571911-A.
01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9619581-A1.
                                                                                                                                                                                                       Synthetic
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                                                                                   Gaps
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Polynucleotides encoding the L and H chains of human anti-HBs Ab are given in Q49944. The Ab can be easily produced in large quantities for therapeutic use.

Sequence 1066 BP; 338 A; 274 C; 240 G; 214 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurihara I, Matsukura S, Nishihara I, Tsuruoka N;
                                         ö
Length 3437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 5.1%; Score 44; DB 8; Length 1066; Best Local Similarity 86.7%; Pred. No. 7.13e-06; Matches 52; Conservative 0; Mismatches 8; Indels
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1994.

02-DEC-1993; AU0617.

03-DEC-1992; AU-006380.

(UNIX ) UNISEARCH LID.

Flores MV, Osullivan WJ, Stewart TS;

WPI: 94-20021/24.

P-PSDB; R55694.

Nucleic acid encoding carbamoyl phosphate synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        062924;
06-DEC-1994 (first entry)
Carbamoyl-phosphate-synthetase II.
Carbamoyl-phosphate-synthetase II; CPSII; psCPSII gene;
                   Pred. No. 3.02e-06;
0; Mismatches 7;
                                                                                                                                                                                                                                 049943;
29-APR-1994 (first entry)
Human anti-HBs light chain.
Antibody; Ab; light; heavy; chain; hepatitis B;
HB; surface antigen; ss.
  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/note= "claim 1, page 26"
Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         malaria; ss.
Plasmodium falciparum.
Location/Qualifiers
Rey
1226..8401
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 33..743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /EC_number = 6.3.5.5
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    MAKAMA MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding allograft rejection factors and immunogenic fragments - useful for identifying transplant rejection inhibitors

useful for identifying transplant rejection inhibitors

Useful for identifying transplant rejection inhibitors

(199372-099393 are rat allograft inflammatory factor 2 (AIF-2) cDNA fragments. The AIF-2 gene is a differentially expressed allograft gene which is expressed in allograft tissue during transplant rejection. Identification of the rat AIF-2 product (R80521) or transcript indicates that allograft rejection is taking place. The rat AIF-2 gene, fragments of this gene and/or the gene product are therefore useful in the diagnostic methods used allow rejection (vascular inflammation) to be detected at an early stage and require only a small amount of
                                                                                                                                                                                                                                                                                                                                                                        560 atttattcatttatttatttttttttttagtttataaaatag-taattctactaatttaa 618
                                                                                                                                                                                                                                                                                                                                                                                                  the treatment of malaria.

Disclosure; Page 6-16; 31pp; English.

The cDNA sequence encoding the carbamoyl-phosphate-transferase II

(CPSII) of Plasmodium falciparum was determined. The cDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSb.

Sequence 8920 BP; 3836 A; 774 C; 1232 G; 3078 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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isolated from Plasmodium falciparum, used to develop prods. for
                                                                                                                                                                                                                                                                                                                          0; Mismatches 21; Indels 1;
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0
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08-FEB-1996 (first entry)
Rat allograft inflammatory factor 2 (AIF-2) cDNA fragment.
AIF-2; allograft inflammatory factor 2; transplant rejection;
inhibitor; immunogenic; detection; diagnosis; ds.
                                                                                                                                                                                                                                                                                 Length 8920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 16; Length 340
Pred. No. 1.67e-05;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 T;
                                                                                                                                                                                                                                                                             Score 44; DB 11; I
Pred. No. 7.13e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               833 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 6
Q99393 standard; cDNA; 340 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 7
Q99380 standard; cDNA; 350 BP.
Q99380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 A;
                                                                                                                                                                                                                                                                             Query Match 5.1%;
Best Local Similarity 76.3%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.0%;
Best Local Similarity 78.7%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-1995.
21-DEC-1994; U14724.
21-DEC-1993; US-171385.
(HARD ) HARVARD COLLEGE.
RUSSELI ME, UTENS U;
WPI; 95-240668/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              805 tgaccacaaataaat 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide 111 as C)
Sequence 340 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biopsy material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
W09517506-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                              DNA encoding allograft rejection factors and immunogenic fragments - useful for identifying transplant rejection inhibitors (laim 11; Page 92; 188pp; English.

Q99372-Q99393 are rat allograft inflammatory factor 2 (AIF-2) cDNA fragments. The AIF-2 gene is a differentially expressed allograft gene which is expressed in allograft tissue during transplant rejection. Identification of the rat AIF-2 product (R80521) or transcript indicates that allograft rejection is taking place. The rat AIF-2 gene, indicates that allograft rejection is taking place. The rat AIF-2 gene, the diagnosis of transplant rejection (vascular inflammation) the diagnostic methods used allow rejection (vascular inflammation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biopsy material (Sequence ID listing in the specification gives
              Rat allograft inflammatory factor 2 (AIF-2) cDNA fragment.
AIF-2; allograft inflammatory factor 2; transplant rejection;
inhibitor; immunogenic; detection; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein synthesis inhibitíng gene.
Plant pathogens; pathogen resistance; medicine;
Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 16; I
Pred. No. 1.67e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= e
/note= "possible polyA signal"
1002..1011
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/note= "possible polyA signal"
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/note= "possible polyA signal"
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20-DEC-1990; 040954.
20-DEC-1990; DE-040954.
(PLAC ) MAX PLANCK GES FORDERUNG WISSE.
Jach G, Logemann J, Mundy J, Schell J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q25785 standard; DNA; 1078 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%;
Best Local Similarity 78.7%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1032..1078
/*tag= g
(first entry)
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886..1078
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930..935
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                                                                                                                                                                              21-DEC-1993; US-171385.
(HARD ) HARVARD COLLEGE.
Russell ME, Utans U;
WPI; 95-240668/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide 111 as C)
Sequence 350 BP;
                                                                                                                                 29-JUN-1995.
21-DEC-1994; U14724
                                                                                       Rattus sp.
WO9517506-A1.
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03-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trecombinant DNA procedures for use as growth promoters for enhancing lactation, for stimulating cell proliferation etc.

Trecombinant DNA procedures for use as growth promoters for enhancing lactation, for stimulating cell proliferation etc.

Example: Fig 5: 59pp. English.

A 42 base oligonucleotide corresponding to the DNA sequence encoding amino acids 10 to 23 of mature human IGF-I was synthesized (N70437).

The radiolabeled 42 mer was then employed to screen for IGF-I containing DNA sequences in a human liver cDNA library. Insulin-Clike growth factors-IA and -IB cDNAs were isolated from a human cDNA library by using lambdagt 11 (N70435, N70436). The human IGF-I genomic gene was isolated and mapped. It encodes at least two preproinsulin-like growth factor-I proteins. An essentially pure proproinsulin-like growth factor-I protein comprising the sequence of amino acids shown in Figure six is claimed (P7037).

Sequence 1136 BP; 412 A; 230 C; 268 G; 226 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                      Pathogen resistant plants prodn. using protein synthesis inhibiting pener or its fusion products, inserted into the genome, also pharmaceutical use of derived synthesis inhibiting protein bisclosure; Fig 3: 23pp; German.

The sequence is that of a gene encoding a protein which effectively blocks protein synthesis by plant pathogens, e.g. Trichoderma reesis and Fusarium sporotrichoides. It can be fused to active promoters such as wun-1 and the fusion introduced into plant genetic material to impart pathogen resistance to both mono- and di-cotyledonous plants. The gene was isolated from mature barley seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      865
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Heterodimeric human interleukin 12 subunit 2 encoding cDNA.
Heterodimeric; human; interleukin 12; IL-12; vaccine; antigen;
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                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1991 (first entry)
Sequence encoding insulin-like growth factor 1B (IGF-1B).
Growth promoter; lactation enhancer; cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krivi GG, Rotwein PS;
WPI; 87-200203/29.
New pre-pro-insulin-like growth factor-1 protein - obtd. by
                                                                                                                                                                                    Length 1078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length 1130;
Pred. No. 1.67e-05;
""" matches 7; Indels
                                                                                                                                                                                    Score 43; DB 4; Length 1078, Pred. No. 1.67e-05; 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                           T 9
N70435 standard; cDNA; 1136 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V15228 standard; cDNA; 1364 BP. V15228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1987.
06-JAN-1987.
07-JAN-1986. US-816662.
20-NOV-1986; US-929671.
(UNIW ) UNIV OF WASHINGTON.
                                                                                                                                                                                    Match 5.0%;
Local Similarity 85.2%;
les 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Match 5.0%;
Local Similarity 87.7%;
nes 50; Conservative
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Immunogenic compsn. to improve cell mediated immune response -
contains soluble leishmania antigen and interleukin-12 as adjuvant
Disclosure; Column 23-26; 22pp; Bnglish.

This is the nuclectide sequence encoding the human interleukin (IL)-12
30 kD subunit. IL-12 is a heterodimeric complex composed of the 30 kD
subunit and a 40 kD subunit (W07398). The complex is used in a novel
immunogenic composition comprising a soluble Leishmania antigen with
IL-12, for protection against leishmaniasis. The addition of IL-12
improves cell-mediated immunity by inducing TH1 helper cells (as opposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin 12; IL-12; beterodimeric complex; immunogenic; ds; Human; interleukin 12; IL-12; beterodimeric complex; immunogenic; ds; Leishmania; antigen; leishmaniasis; cell.mediated immunity; adjuvant; TH1 helper cell; TH2 helper cell; alum; cytokine; bacterium; cancer; vaccine; cell surface; membrane; qlycoprotein; antigen presenting cell.
                                                                                                                                                                     /product= "heterodimeric human interleukin 12 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIL-12) subunit (putatively the 30 KD subunit) shown in the present specification. The present invention describes a method for enhancing the immune response elicited by an antigenic composition. The method antigenic composition. The IL-12 simultaneously or sequentially with the antigenic composition. The IL-12 can be used in therapeutic compositions, e.g. as an adjuvant in vaccines against pathogenic bacteria or viruses, especially in an amount of 0.1 mu g to 0.5 mg per Sequence 1364 BP; 446 A; 282 C; 275 G; 361 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhancing immune response to vaccine - comprises co-administering interleukin-12 with antigenic composition bisclosure; Column 2-26; 23pp; English.

The present sequence encodes a heterodimeric human interleukin 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
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0; Mismatches 5; Indels
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ġs.
pathogen; immune response; microorganism; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 40;
                                                                                                                                                                                                                                                                                                    17-JUN-1994; US-265087.
18-APR-1994; US-229282.
25-MAR-1996; US-621493.
(UYPE-) UNIV PENNSYLVANIA.
(WIST-) WISTAR INST ANATOMY & BIOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-1994; US-229282.
17-UOW-1994; US-265087.
(UYBE-) UNLY PENNSYLVANIA.
(WIST-) WISTAR INST ANATOMY & BIOLOGY.
Scott P. Trinchieri G;
WPI: 96-503347/50.
P-PSDB: W07399.
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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T48099 standard; cDNA; 1364 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%;
Best Local Similarity 90.6%;
Matches 48; Conservative
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21-MAR-1997 (first entry)
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                                   Homo sapiens.
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RESULT
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to TH2 cells which are induced by alum adjuvant) and does not cause uncontrolled release of other cytokines (in contrast to bacterial adjuvants). IL-12 can also be used as a cancer vaccine by association with the protein B7, a soluble, cell-surface (membrane)-bound glycoprotein which is expressed in antigen presenting cells. Sequence 1364 BP; 446 A; 282 C; 275 G; 361 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                024371;
16-SEP-1992 (first entry)
Natural killer cell stimulatory factor 30kD subunit.
NKSF: cytokine; gamma interferon; IFN; peripheral blood lymphocytes;
IL-2; GM-CSF; granulocyte macrophage colony stimulating factor; PBL;
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New natural killer cell stimulatory factor - useful as an immunostimulant for inducing gamma-interferon and GM-CSF prodn. In human peripheral blood lymphocytes.

Claim 12; Page 23; 79pp; English.

NKSF is capable of inducing the production of gamma interferon in human peripheral blood lymphocytes. It has subunits of 40 (R22769) and 30-35 kD (R23729). It is claimed that NKSF is useful in the treatment of bacterial and viral infections e.g. AIDS.

Degenerate probes were designed from tryptic fragments of NKSF and used to screen a CDNA library made from poly A RNA from PGBu induced 8866 cells to identify a cDNA encoding the small subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/label= p35nksf9-1-1
/note= "short clone containg 30kD NKSF subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/label= p35nksf14-1-1
/note= "long clone containing 30kD NKSF subunit"
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                                                                                                                                                                      Score 43; DB 26; Length 1364;
Pred. No. 1.67e-05;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 4; Length 1396;
Pred. No. 1.67e-05;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WIST-) WISTAR INST.
Clark S C, Hewick R, Kobayashi M, Perussia B, Trinchieri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= pro NKFS 30kD subunit
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14..1364
                                                                                                                                                                                                                                                                                                                                                                                      n 12
Q24371 standard; DNA; 1396 BP
                                                                                                                                                                      Query Match 5.0%;
Best Local Similarity 90.6%;
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Local Similarity 90.6%;
les 48; Conservative
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                                                                                                                                                                                                                       48; Conservative
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18-SEP-1990; US-584941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92-132124/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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LT 13 Q10896 standard; DNA; 1558 BP.

RESULT ID 010

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claim 3; Page 13-17; 34pp; English.

Claim 3; Page 13-17; 34pp; English.

CDNA libraries were constructed from the mouse osteoblastic cell
line MC3T3-El and from mouse liver tissue, amplified by PCR, and
then as much common DNA as possible removed by hybridisation between
the 2 libraries. Residual El-specific DNA was amplified, inserted
into lambda gt10 and screened by plaque hybridisation. A minibank of
                                                                                                                                                                                                                                                                                                                                                                        used in therapy of fracture or osteoporosis claim 5; Fig 2; 28pp; English.
A Xenopus laevis unfertilised of Communication of X.laevis Xar14 chromosomal DNA. Three clones were isolated, including clone Xbr23 which was found to encode a protein having homology with X.laevis BMP-2B. They were subcloned in pUC19 and used to transform competent E.coli HB101 cells. Transformant E.coli HB101/pXbr23 coding for the BMP-2B was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           044391;
14-SEP-1994 (first entry)
Sequence of murine OSF-4 cDNA.
OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis bone morphogenetic protein and DNA encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2; Length 1558; Pred. No. 1.67e-05; 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsujimura A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bone related, cadherin-like OSF-4 proteins – for trea and diagnosis of bone metabolic disease, and nucleic acid
13-MAY-1991 (first entry)
Encodes Xenopus Bone Morphogenetic Factor BMP-2B.
BMF; osteoporosis; fracture; cartilage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okazaki M, Takeshita S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 14
Q44391 standard; cDNA to mRNA; 3581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                              Location/Qualifiers
                                                                                                                                       /product= BMP-2B
                                                                                                                                                                                                                                                         (TAKE) TAKEDA CHEMICAL IND KK. (SCIT-) SCITECH RESEARCH CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequenced.
See also Q10890-5 and Q10897.
Sequence 1558 BP; 504 A;
                                                                                                                                                                                                                                                                                             Murakami K, Ueno N, Kato Y;
WPI; 91-075112/11.
P-PSDB; R10996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.2%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-1993; 113602.
28-AUG-1992; JP-230028.
(FARH ) HOECHST JAPAN LTD.
Amann E, Kawai S, Okazak
                                                                                                                                                                                                                06-SEP-1989; JP-229250.
20-JUL-1990; JP-190774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                       /*tag=
                                                                                                                                                                                              05-SEP-1990; 117079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 94-076152/10.
P-PSDB; R49730.
                                                          Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-585801-A
                                                                                                                                                         EP-416578-A
                                                                                                                                                                              13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1527 a 1527
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This sequence is the 3' portion of clone H1075_1, which is a polynectoride of the invention. This sequence was isolated from a human peripheral blood monoucleocyte (PBWC) CDNA library. The polynucleotide, which encodes a secreted protein, can be used, e.g. as a tissue or molecular weight marker, in genetic fingerprinting, to raise anti-protein or anti-DNA antibodies and in interaction trap assays. The protein can be used to assay biological activity, raise antibodies for use in munoassays, as a marker, to identify inhibitors of its interactions and as a nutritional supplement. It may also have a very wide range of the rapecutic and biological activities (no examples are given to support this), e.g. cytokine or modulator of cell proliferation and differentiation, immunostimulator of cell proliferation and differentiation, immunostimulator, chamnosuppressant, haematopoiesis stimulator, follicle inhibitory/stimulator, chemotactic/chemokinetic, haemostatic, thrombolytic or anti-inflammatory agent, antimicrobial, borned and the property agent, antimicrobial, or psoriasis treatation or behaviour modifier, anti-depressant or analgesic companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAY-1998 (first entry)
3' fragment of clone H1075.1.
Human; secreted protein; molecular weight marker; genetic fingerprinting; antibody production; nutritional supplement; therapy; clone H1075_1; peripheral blood mononucleocyte; PBMC; ds.
                                                                                                                                                                                                                                                                                                        ö
             used to screen total RNA from both cell types. One clone specific for El was identified and sequenced. The insert from this clone was used to screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced, it encoded the 796 AA mouse precursor protein (Q44391/R49730). The insert was also used to screen a cDNA bank prepd. from human osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and OSF-4-2 (Q44392/R49731 and Q44393/R49732
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.91e-05;
0; Mismatches 15; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid clones from ATCC 98028 encode novel secreted proteins - having many potential uses, e.g. as immunomodulators, cell proliferation or differentiation inhibitors or haematopoiesis regulators
E-specific clones was recovered, their inserts amplified and
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                  886 T;
                                                                                                                                                                                                                                                          Length 3581;
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                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs K, Lavallie ER, Mccoy JM, Merberg D, Racie LA,
                                                                                                                                                                                                                  800 G;
                                                                                                                                                                                                                                                     f. Match 5.0%; Score 43; DB 10; I Local Similarity 90.6%; Pred. No. 1.67e-05; les 48; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 G;
                                                                                                                                                                                                                  774 C;
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                                                                                                                                                                                                                1121 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 15
V00423 standard; cDNA; 259 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.7%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-1997,
14-APR-1997; U06134,
19-APR-1996; US-635311.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                3581 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 97-535776/49.
                                                                                                                                                                                            respectively
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Search completed: Tue Dec 15 19:01:29 1998 Job time : 216 secs.

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1.67e-06
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sequence 17, Application Sequence 5, Application Sequence 6, Application Sequence 11, Application Sequence 11, Application Sequence 124, Application Sequence 124, Application Sequence 124, Application Sequence 124, Application Sequence 13, Application Sequence 14, Application Sequence 14, Application Sequence 17, Application Sequence 18, Applic

US-08-484-US-08-628-US-08-341-US-08-355-US-08-355-US-08-300-US-08-300-US-08-300-US-08-300-US-08-300-US-08-300-US-08-1176-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1143-US-08-1144-US-08

(WE)	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	O
MPsrch_nn n.a n.a. database search, using Smith-Waterman algorithm Run on: Tue Dec 15 19:01:47 1998; MasPar time 34.86 Seconds	υ
1157.525 Million cell updates/sec Tabular output not generated.	
Title: >US-09-109-864-1 Description: (1-865) from USO9109864.seq Perfect Score: 865 I tttgtggagggcagcagagaaaaaaaaaaaaaaa	
Scoring table: TABLE default Gap 6	RESU
Nmatch STD : Dbase 0; Query 0	DT
Searched: 88822 segs, 23323279 bases x 2	3 C E
Post-processing: Minimum Match 0% Listing first 45 summaries	288
Database: n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1	888
Statistics: Mean 8.740; Variance 6.833; scale 1.279	등
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	38888
SUMMARIES	388
Result Query No. Score Match Length DB ID Description Pred. No.	3888

ALIGNMENTS

RESULT

AC 08-232-463-14 STANDARD; DNA; UNC; 7218 BP.

AC XXXXX

DE Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
CC GENERAL INFORMATION:
CC GENERAL INFORMATION:
CC APPLICANT: FOREST.
CC APPLICANT: SCHETFLINGER, F.
CC APPLICANT: SCHETFLINGER, F.
CC APPLICANT: SCHETFLINGER, F.
CC APPLICANT: SCHETFLINGER, F.
CC APPLICANT: PALENTRER, F. G.
CC TITLE OF INFURTION:
CC TITLE OF INFORMATION:
CC COUNTER: 1080 Diagonal Road, Suite 500
CC COUNTER: 1080 PRACE COUNTER: 1080
CC COUNTER: 1080 PROPERIOR
CC CASSIFICATION NUMBER: 05/07/935,313
CC CASSIFICATION NUMBER: 26-AUG-1991
CC REDEPONDE: (703)863-9300
CC TELERA: 89914 PROPERATION
CC REDEPONDE: (703)863-9300
CC INFORMATION FOR SEQUENCE

9.26e.09 2.65e.08 2.65e.08 2.65e.08 7.55e.08 7.5

Sequence 14, Applicati Sequence 27, Applicati Sequence 14, Applicatio Sequence 17, Applicatio Sequence 14, Applicatio Sequence 14, Applicatio Sequence 16, Applicatio Sequence 16, Application Sequence 16, Applicatio Sequence 16, Applicatio Sequence 1, Applicatio

7218 3218 3218 320258 300733 300733 30033 310333 310333 310333 310333 310333 310333

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PCT-US95-0 US-07-642-US-08-104-US-08-174-

US-08-261-US-07-602-5258287-23

US-08-232-US-08-171-US-08-171-US-08-265-US-08-232-US-08-08-455-US-08-08-09-US-08-08-132-US-08-08-132-US-08-131-US-08-131-US-08-131-US-08-131-US-08-131-US-08-131-US-08-131-US-08-131-US-08-199US-09-109-864-1.rni

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RESULT
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                                                                                                                                       685 cagatggagccatatcccaggctcctggtggaggaaggtgcagagttcgaggaacctttg 626
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                                                                                                                  Gaps
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                      625 cactettgtgccttccctcaggcccaaagctcctgtagactcagtctcgt 576
                                                                                          Query Match 5.1%; Score 44; DB 1; Length 7218; Best Local Similarity 0.7%; Pred. No. 9.26e-09; Matches 2; Conservative 165; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08171385
Sequence 27, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSPER: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TIPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55X
OPPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                 77 2
US-08-171-385-27 STANDARD; DNA; UNC; 340 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
LENGIH: 7218 base pairs
           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                   TOPOLOGY: line:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
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                                                                                                                                                                          Query Match

5.0%; Score 43; DB 1; Length 340;
Best Local Similarity 78.7%; Pred. No. 2.65e-08;
Matches 59; Conservative 0; Mismatches 16; Indels
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Pred. No. 2.65e-08;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mary E. Russell
APPLICANT: Wary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE 340 BP; 114 A; 38 C; 64 G; 124 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE 350 BP; 121 A; 37 C; 63 G; 129 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02110-2804
COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
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US-08-171-385-14 STANDARD; DNA; UNC; 350 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08171385
Sequence 14, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/POCKET NUMBER: 0542
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,819
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TELEEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-5070
(617) 542-8906
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.0%;
Best Local Similarity 78.7%;
Matches 59; Conservative
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STATE: Massachusetts
COUNTRY: U.S.A.
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                     805 tgaccacaaataaat 791
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                                               LENGTH: 340
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GENERAL INFORMATION:
APPLICANT: DORNER, F.
                                                                                                                                                           USA
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TELEX: 200291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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Sequence 3, Application US/08265087
Patent No. 5571515
GENERAL Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.0%; Score 43; DB 1; Length 1364; Best Local Similarity 90.6%; Pred. No. 2.65e-08; Matches 48; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                         ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 101..859
SEQUENCE 1364 BP; 446 A; 282 C; 275 G; 361 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                             ZIP: 19477

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 5
US-08-455-550-7 STANDARD; DNA; UNC; 1558 BP.
                                                                                                    JT 4
US-08-265-087-3 STANDARD; DNA; UNC; 1364 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                        MOLECULE TYPE: CDNA
                                           62 TAGCCATAATGAAAT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                         XXXXXX
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| Sequence 7, Application US/0845550
| Sequence 7, Application US/0845550
| CREMENAL INCOMPATION
| CONTRICT | CANADATION | CREMENAL INCOMPATION
| CONTRICT | CANADATION | CREMENAL INCOMPATION | CREMEMATION |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 ctccttcgcagacagaactctggcctggatctcccgctggggggagaagaagtctc 266
                                                                                                                                                                                                                                                                                                                                                                                                                                77 agctggacatcctttcctgctgatgagccccaggctggaggtgccctgctcacatgctct 86
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 agccccttcctcttttacccccagagattctttgaggtgctgctcctgttcc 319
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                  Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                  5.0%; Score 43; DB 1; Length 7218
Similarity 2.4%; Pred. No. 2.65e-08;
7; Conservative 161; Mismatches 125; Indels
                                                                             COUNTRY: USA
ZIP: 22313-0299
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
YMMER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 36-AUG-1991
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/COCKET NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JT 7
US-07-688-352C-31 STANDARD; DNA; UNC; 3073 BP
                                           ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/07688352C
                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                       ٧A
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
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APPLICANT: Wigler, Michael H.
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30, Application PC/TUS9102714
Sequence 30, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Wigher, Michael H.
APPLICANT: Colicelli, John J.
TILLE OF INVENTION: Clouing by Complementation and Related
TITLE OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 1; Length 3073;
Pred. No. 7.52e-08;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FILPOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CONFIGNATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING APPLICATION WHEER: US 07/511,715
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN MICHAEL F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEPHONE: CARACTERISTICS:
LENGTH: SAUTH STORMATION:
REGISTRATION STORMATION:
TELEPHONE: CARACTERISTICS:
LENGTH: SAUTH STORMATION:
TELEPHONE: MICHAEL STORMATION:
TELEPHONE MICHAEL STORMATI
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 3..1111
SEQUENCE 3073 BP; 897 A; 684 C; 635 G; 857 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 8
PCT-US91-02714-30 STANDARD; DNA; UNC; 3073 BP.
Sequence 31, Application US/07688352C Patent No. 5527896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.9%;
Best Local Similarity 88.9%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Ouery Match

4.7%; Score 41; DB 3; Length 688;

Best Local Similarity 83.6%; Pred. No. 2.13e-07;

Matches 51; Conservative 0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1900
Patent No. 5498694.
Patent No. 5498694
APPLICANT: RUOSLAHTI,ERKKI I.
TITLE OF INVENTION: PEPTIDES OF THE CYTOPLASMIC DOMAIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.7%; Score 41; DB 2; Length 198;
Best Local Similarity 83.6%; Pred. No. 2.13e-07;
Matches 51; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:3:
LENGTH: 688
Sequence 745 BP; 234 A; 132 C; 157 G; 165 T; 57 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 8D4-T3
SEQUENCE 198 BP; 87 A; 20 C; 23 G; 68 T; 0 OTHER.
CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION DATA:
APPLICATION DATA:
TOTALOR DATE: 07/796,066
FILING DATE: 20-NOVEMBER-1991
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, GIULIO A. Jr.
REFERENCE/DOCKET NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-028PC
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-227-440
TELEFAX: 617-227-544
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TENCHMUNICATION DATE: SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,967
FILING DATE: 10-MAY:
APPLICATION DATA:
APPLICATION NUMBER: 973,547
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: 357,824
FILING DATE: 25-MAY-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 10
5498694-3 STANDARD; DNA; UNC; 745 BP.
                                                                                                                                                                                                                                                LENGTH: 198 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
CELL TYPE: T-cell blast
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 A 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.9%; Score 42; DB 2; Length 3073; Best Local Similarity 88.9%; Pred. No. 7.52e-08; Matches 48; Conservative 0; Mismatches 6; Indels
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMUTER: IBM FC Compatible
OPERATIC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/COCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEFONE: (312) 346-5750
TELECOMMUNICATION INFORMATION:
TELEFONE: (312) 944-9740
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3073 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 3..1111
SEQUENCE 3073 BP; 897 A; 684 C; 635 G; 857 T; 0 OTHER.
   STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application PC/TUS9210087
Sequence 16, Application PC/TUS9210087
GENERAL INFORMATION:
APPLICAMT: Smith, Kendall A.
TITLE OF INVENTION: IL-2-Stimulated Gene
TITLE OF INVENTION: Expression
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 9
PCT-US92-10087-16 STANDARD; DNA; UNC; 198 BP.
XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
COUNTY: Boston
COUNTY: U.S.A.

ID: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10087
FILING DATE: 19921118
                                                                                           ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     CLITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP.
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RESULT

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Sequence 4, Application US/08361467B
Sequence 4, Application US/08361467B
C Patent No. 5633441
C GENERAL INFORMATION:
APPLICANT: Van Emmelo, John
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Oliveria, Dulce E.
APPLICANT: De Oliveria, Maria-Helena
APPLICANT: De Oliveria, Maria-Helena
APPLICANT: De Oliveria, Maria-Helena
APPLICANT: De Oliveria, Maria-Helena
APPLICANT: De SOUZA, MARIA-HELE
TITLE OF INVENTION: EMBRYOS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 1046; Pred. No. 2.13e-07; 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA IMMEDIATE SOURCE: CLONE: 3C9 SEQUENCE 1046 BP; 360 A; 254 C; 166 G; 266 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/361,467B
FILING DATE: 22-DEC-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 04-AUG-1989
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,196
REGISTRATION NUMBER: 31,196
REGISTRATION NUMBER: 31,196
REGISTRATION NUMBER: 31,196
REGISTRATION NUMBER: 31,096
REGISTRATION FOR SEQ ID NO: 4:
SEQUENCE CHARRACTERISTICS:
LEGGTH: 1046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1008 AAAAAAAAAAAAAA 1026
                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.9%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
RESULT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: DATE: PC COMPATIBLE
COMPUTER: PATENTIN DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: O6 NG 1996
CLASSIFICATION
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ANDORNEY/ABCTI INCOMATION:
MAND: PROGRET INCOMATION:
MAND: PROGRET INCOMATION:
MAND: PROGRET INCOMATION:
MAND: PROGRET INCOMATION:
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4.7%; Score 41; DB 2; Length 2589;
Best Local Similarity 83.6%; Pred. No. 2.13e-07;
Matches 51; Conservative 0; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08199776
Sequence 1, Application US/08199776
Sequence 1, Application US/08199776
Patent No. 5594120
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 5594120el integrin alpha subunit NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: Callfornia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
SEQUENCE 2589 BP; 844 A; 436 C; 522 G; 787 T; 0 OTHER.
                                                                               Sequence 1, Application PC/TUS9612860
Sequence 1, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brezzer, David J.

REGISTRATION NUBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
7T 12
PCT-US96-12860-1 STANDARD; DNA; UNC; 2589 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
ID US-08-199-776-1 STANDARD; DNA; UNC; 3933 BP.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02044
FILING DATE: herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/199,776
FILING DATE: 18 February 1994
ATTORNEY/AGENT INFORMATION:
NAME: REDIECTION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3933 base pairs
TYPE: NUCLEIC ASINGLE
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: 180..3659
FEATURE:
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    COUNTRY: USA ZIP: 02210
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ANTI-SENSE: N
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Pred. No. 2.13e-07;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: sig_peptide
LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9502044
Sequence 1, Application PC/TUS9502044
GENERAL INFORMATION:
APPLICANT:
TILLE OF INVENTION: Novel integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
ADDRESSEE: Wolf, Greenfield and Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /I 14
PCT-US95-02044-1 STANDARD; DNA; UNC; 3933 BP.
                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGIGTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-3441
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
CELL TYPE: mucosal lymphocyte
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide LOCATION: 180..3659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.7%;
Best Local Similarity 78.9%;
Matches 56; Conservative
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LOCATION: 126..3662
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                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMC
                                                                                                                                      FILING DATE:
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Sequence 1, Application US/07642002
Sequence 1, Application US/07642002
Sequence 1, Application US/07642002
Sequence 10. Sef8465
Sequence 10. Sef8465
September 10. Sef8465
September 10. Sef8465
September 10. Sept
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NAME/KEY: sig_peptide
LOCATION: 126..179
SEQUENCE 3933 BP; 938 A; 1062 C; 1074 G; 859 T; 0 OTHER.
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US-07-642-002-1 STANDARD; DNA; UNC; 5108 BP.
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NAME/KEY: CDS
LOCATION: 400.4686
OTHER INFORMATION:
SEQUENCE 5108 BP; 1220 A; 1491 C; 1368 G; 1029 T; 0 OTHER.
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Pred. No. 2.13e-07;
0; Mismatches 1; Indels
                                        CITY:

STATE:

CONDUTRY:

COMPUTRY:

COMPUTER:

COMPUTER:

CONFOUTER:

COMPOTER:

CONFOUTER:

CONFOUTE
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
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Best Local Similarity 97.7%;
Matches 42; Conservative
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Search completed: Tue Dec 15 19:02:31 1998 Job time: 44 secs.

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Gaps ; 0

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Release 3.1A John F. Collins, Biocomputing Research Un. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 5.62 Seconds 382.814 Million cell updates/sec Tue Dec 15 15:53:21 1998; MPsrch_pp

not generated. Tabular output >US-09-109-864-2 (1-133) from US09109864.pep Description: Perfect Score: Sequence:

1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133 PAM 150 Gap 11 Scoring table:

131922 seqs, 16180660 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq32
lipart1 2.part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
24:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28

Mean 30.678; Variance 131.480; scale 0.233 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
		dР					
Result		Query					
No.	Score	Match	Match Length DB	BB	Di .	Description	Pred. No.
-	140	14.3	317	19	W03519	Prostate carcinoma tu	2.28e-03
7	109	11.1	316	13	R75702	Rat galectin-8.	7.19e-01
m	92	9.4	278	13	R72597	Ostertagia protective	1.41e+01
7	88	9.1	323	53	W46883	Protein sequence enco	2.34e+01
ß	89	9.1	323	23	W11841	Human galectin-4-like	2.34e+01
9	88	9.1	323	20	W06551	Human colon specific	2.34e+01
7	89	9.1	343	56	W36070	E. coli DNA polymeras	2.34e+01
60	88	9.1	983	13	R75761	BAV3 ORF6-encoded pro	2.34e+01
σ	87	8.9	343	œ	R40125	DNA polymerase III ho	3.27e+01
10	82	8.7	311	28	W36129	SnpR activator protei	4.56e+01
11	82	8.7	495	~	R07143	Neuronal nicotinic ac	4.56e+01
12	84	8.6	212	10	R54922	cdil polypeptide.	5.38e+01
13	84	8.6	704	13	W01102	Signal transducer and	5.38e+01
14	84	8.6	748	13	W01101	Signal transducer and	5.38e+01
15	83	8.5	264	m	R12531	Mac2.16 expression pr	6.34e + 01
16	83	8.5	278	m	R13338	Mac-2 protein includi	6.34e+01
17	83	8.5	687	23	W22458	Yeast wild-type aceto	6.34e + 01
18	83	8.5	687	-	P81152	Herbicide sensitive,	6.34e+01

6.34 e+ 0.01
Chicken oocyte recept Anti-1ysozyme VH. IL-4 Stat peptide. Yeast transcription T. niveum Cyclosporin Canine gastric lipase DOG gastric lipase Preast mitochondria CO MOUSE TRADD intracell Human NF-ATP. Pyruvate oxidase (P17 Pyruvate oxidase (P17 Pyruvate oxidase (P17 Pyruvate oxidase (M18 Human alpha-2 macrogl LK26 humanised VH reg Cytochrome P450 homol HL-60 and placenta le Human GBP. Human GBP. H. Pylori transmembra Peptide fragment of m TATA-binding protein TATA-binding protein Human TATA-binding protein Publica Fatagent Patra Patr
R43827 R43827 R13826 R13826 R44929 R56870 R56871 R56871 R56871 R05330 R60255 R05730 R02248 R11749 R02248 R12749 R22625 R42831 R22625 R42831 R22625 R42831 R22625 R42831 R22625 R42831 R22625 R42831 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R42642 R4493 R42642 R4493 R4
13 22 22 22 22 23 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25
863 1123 1220 1220 1220 1320 1320 1484 11484 1135 1135 1135 1135 1135 1135 1135 113
88 88 11 11 11 12 12 12 12 12 12 12 12 12 12
0011284888888888888888888888888888888888

ALIGNMENTS

DNA encoding prostate carcinoma tumour antigen and prostate tumour PT inducing genes - and related proteins, vectors, antibodies, etc., for diagnosis and treatment of metastatic cancer Disclosure; Fig 18A; 169pp; English.

Disclosure; Fig 18A; 169pp; English.

PCTA (W03519) that is a putative tumour associated antigen present on prostate cancer cells. Its amino acid sequence was deduced from a cDNA clone (T37414) isolated from human prostatic carcinoma is a method for producing MADs specific for cell surface-expressed nolecules. PCTA is a new member of the galectin family, galectin-8. Antibodies raised against PCTA are useful for the detection of metastatic cancer. Cpds. that inhibit PCTA can be sequence 317 AA; Prostate carcinoma tumour antigen.
Prostate carcinoma tumour antigen, PCTA-1; oncogene; candiagnosis; therapy; metastasis; cell surface expression; surface epitope masking; galectin-8. T 1 W03519 standard; Protein; 317 AA. 18-JUL-1996. 11-JAN-1996; U00307. 11-JAN-1995; US-371377. (UYCO) UNIV COLUMBIA NEW YORK. Fisher PB. Shen R; WPI, 96-342235/34. N-PSDB; T37414. 26-NOV-1996 (first entry) Homo sapiens. WO9621671-A1. RESULT NAME DATE OF THE PROPERTY OF T

Score 140; DB 19; Length 317; Pred. No. 2.28e-03; 41; Mismatches 56; Indels 7; Gaps 14.3%; 24.6%; Query Match 14.3%; Best Local Similarity 24.6%; Matches 34; Conservative

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SPRLEVPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSL-RDQAAHAPVTLRASFADRTL 60

셤 δ 240 vrnsflqeswgeeernitsfpfspgmyfemilycdvrefkvavngvhsleykhrfke-1s 298 : | : | | : | | : | : | : | 셤

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(UYME ) UNIV MELBOURNE
                             086743
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
US5733748-A.
                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                W46883;
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61 AWIS--R--WGQKKLISAPFLFYPQRFFEVLLLFQEGGLKLALNG-QGLGATSMNQQALE 115
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                                                                                                                                                                                                                                                                                                                                        Galectin-8 and corresp. DNA - used in regulation of cell growth, esp.
inhibition of cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RLEVPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSL-RDQAAHAPVTLRASFADRTLAW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CDNA encoding galactin-8, a novel 35 kDa S-type lectin, was cloned when a lambda ZAP II rat liver cDNA library was screened with antibodies directed against the C-terminal end of IRS-1.

Recombinant galectin-8 was expressed in E. coli and CHO cells.

Sequence 316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                          175.316
/label= CBD
/note= "C-terminal carbohydrate recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ostertagia protective antigen.
Protective antigen: parasite; immunogen; vaccine; lectin; beta-galactoside binding protein.
Ostertagia circumcincta.
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 109, DB 13; Length 31
Pred. No. 7.19e-01;
41; Mismatches 58; Indels
                                                                                                                  Galectin-8; lectin; antiproliferative; antitumor.
                                                                                                                                                                                                Linker_peptide
                                                                                                                                        Location/Qualiflers
                                                                   .m 2
R75702, standard; Protein; 316 AA.
R75702;
14-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 278 AA.
                                                                                                                                                                                                                                                                                                  YEDA RES & DEV CO LID.
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116 OLRELRISGSVOLYCVHS 133
                                                                                                                                                          /label- CBD
                                                                                                                                                                                                                                                                                                                                                                                                                              Match 11.1%;
Local Similarity 22.1%;
les 30; Conservative
                                                                                                (first entry)
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/label- L
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                   299 sidtleingdihllevrs
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05-DEC-1994; U13679.
05-DEC-1993; IL-107880.
                                                                                                                                                                             domain"
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28-SEP-1993; AU-001494.
(MEAT-) MEAT RES CORP.
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                                                                                                         Rat galectin-8
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                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                 (YEDA )
Zick Y;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                       (RYCU/)
                                                                                                                                                                                       peptide
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                                                                               Protective antigens against Ostertagia, Trichostrongylus and Fasciola species - are isolated by a method involving the use of antibody probes from immune, challenged animals

Disclosure; Fig. 19; 55pp; English.

A CDNA library prepared from 3rd stage larvae of O. circumcincta was screened with a MAD raised against a 32-36 'doublet' antigen identified by Western blotting. Clone specificity was determined by plaque immunoassays, and clones were rescued into the plasmid form (pwOSELOX) by plating on E. coll BM25.8 cells. Clones 3-2 and 5-2b contained identical DNA sequences (given in Q86743) encoding a lectin-like beta-galactoside-binding protein (R72597).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claim 1; Fig 9; 51pp; English.
W46876-80 and W4682-85 represent proteins encoded by colon-specific genes. The polynucleotides encoding these proteins can be used as probes to detect expression of the corresponding human genes, e.g. in diagnostic assays for detecting micrometastases of colon can Recombinant cells containing the polynucleotides can be used to produce the proteins, in order that antibodies can be raised and used in further screening or diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colon-specific nucleic acids - useful as probes for detecting colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSLR-DQAAHAPVTLRASFADRTLAW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1998 (first entry)
Protein sequence encoded by a colon-specific gene.
Colon-specific gene; probe; detection; expression; human;
diagnostic assay; colon cancer; antibody; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 2.34e+01;
36; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92; DB 13; Le
Pred. No. 1.41e+01;
14; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ipyrskltepfepgqtltvkgktgedsvrftinlhnssa 47
   ņ
   Walker
   Newton SE,
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ID W11841 standard; Protein; 323 AA.
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W46883 standard; Protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.4%;
Best Local Similarity 28.2%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.1%;
Best Local Similarity 24.8%;
Matches 33; Conservative
Meeusen ENT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1998.
06-JUN-1995; 469667.
06-JUN-1995; US-469667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cançer micrometastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 leiggdvtlsyvg 322
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                         95-147391/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen C, Yu G;
WPI; 98-229823/20.
N-PSDB; V16676.
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16-MAR-1998 (first entry)
E. coli DNA polymerase III delta subunit protein sequence.
Delta subunit; E. coli; DNA polymerase III holoenzyme; probe; enzyme;.
hybridisation; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The E. coli polymerase III subunits (theta, chi, psi, delta and delta' (198151-198155 respectively)) are used to make man-made enzymes comprising 5 or 6 subunits and potentially for use in long chain PCR. Sequence 343 AA;
                                                                     vpyfgrlqggltarrtiiikgyvpptgksfainfkvgssgdialhinprmgngtvvrnsl 251
                                                                                                                                                          252 lngswgseekkithnpfg--pgqffdlsircgldrfkvyangqhlfdfahrlsafqrvdt 309
                                                                                                                                                                                 7 VPCSHALPQGLSPGQVIIVRGLVLQEPKHFTVSLR-DQAAHAPVTLRASFADRTLAW--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 hilgg1r1ggsepvil1rt1-gre1-111vn1krgsahtp--1ra1f-dkhrvwgnrrg 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 97-470038/43.

N-PSDB; T98154.
Isolated theta, chi, psi, delta and delta' protein sub:units of E. coli polymerase III holo:enzyme - used to make man-made enzyme of 5 coli polymerase III holo:enzyme - used to make man-made enzyme of 5 coli bolymerase III holo:enzyme - used to make man-made enzyme of 5 coli in 17; Column 11-14; 65pp; English.

This is the amino acid sequence of the delta subunit of the E. coli DNA polymerase III holoenzyme. The gene sequence was isolated from a lambda phage library using probes based on the sequences of the tryptic peptides W36072-W36075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%; Score 89; DB 26; Length 343; larity 39.0%; Pred. No. 2.34e+01; Conservative 14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R/5761;
11-NÓV-1995 (first entry)
BAV3 ORF6-encoded protein.
BAV3; vector; veccine; gene therapy; fiber protein.
Bovine adenovirus type 3.
Location/Qualifiers
    Pred. No. 2.34e+01;
36; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= N-glycosylation_site 103..105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= N-glycosylation_site 221..223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by GAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "encoded by GCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   W36070 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R75761 standard; Protein; 983 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUL-1994; 279058.
22-JUL-1994; US-279058.
22-JAN-1993; US-826926.
CORR ) CORNELL RES FOUND INC.
larity 24.8%;
Conservative
                                                                                                                                                                                                                                               310 leiggdvtlsyvg 322
                                                                                                                                                                                                                                                                                           120 LRISGSVQLYCVH 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 239
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nes 23; Conser
  Best Local Similarity
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon specific genes and their expression products - detection of which, in non-colon tissue samples, can be used as indication of colon cancer metastasis.

Tolon cancer metastasis.

Claim 8: Fig 9: 60pp: English.

Novel polypeptides (W06545-53) are encoded by cDNA clones (see also 14580-92) corresponding to 13 human colon specific genes, designated CSG1, CSG2, etc., that are primarily expressed in tissues derived from the colon. Recombinant CSG polypeptides can be produced in transformed host cells. They are useful diagnostic markers for colon cancer and for colon cancer metastasis and can also be used to screen for (ant)agonist cpds. of therapeutic or diagnostic value. Antibodies raised against the colon-specific polypeptides may be used to target colon cancer cells or as part
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
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63 IS-RWG--QKKLISAPFLFYPQRFFEVLLLFQEGGLKLALNGQGLGATSMNQQALEQLRE 119
                                                                                                                                                                                                                                                                                                                                                                            This sequence is a human galectin 4 (a lactose-binding protein)-like protein. The protein, which is expressed specifically in the human stomach and intestines, binds lactose and is useful as a drug and as reagent for research involving carbohydrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 vpyfgrlqggltarrtiiikgyvpptgksfainfkvgssgdialhinprmgngtvvrnsl 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 lngswgseekkithnpfg--pgqffdlsircgldrfkvyangqhlfdfahrlsafgrvdt 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      Kamata K, Kato S, Sekine S, Yamaguchi T;
WPI: 97-119046/11.
N-PSDB: T59539.
Recombinant human galectin 4-like protein and gene - has lactose-binding ability, used in research involving carbohydrate(s) Claim 1; Page 13-16; 25pp; Japanese.
             20-0cr-1997 (first entry)
Human galectin-4-like protein.
galectin-4; lactose binding; stomach; intestine; reagent; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997 (first entry)
Human colon specific gene CSG9 complete polypeptide.
Colon specific gene; CSG9; colon cancer; metastasis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 323;
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Pred. No. 2.34e+01;
36; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                     30-JAN-1997.
09-JUL-1995; JP-174778.
(SAGA) SAGAMI CHEM RES CENTRE.
(SAGA) SAGAMI CHEM RES CENTRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "T 6
W06551 standard; Protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Yu G;
WPI; 97-043054/04.
N-PSDB; T45888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.1%;
Best Local Similarity 24.8%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; antibody; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a colon cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-1996.
06-JUN-1995; U07289.
06-JUN-1995; WO-U07289.
                                                                                       research; carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 leiggdvtlsyvg 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9639419-A1.
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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Gaps

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136 hldvafvhevegslrvpeglrvrvlvqrep-qf-vcl--padh-paaeatsyasptwp-t 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure: Fig 6: 59pp; English.

This protein is the encoded product of the Streptomyces snpR activator gene. The snpR activator gene is incorporated in novel plasmid pANT195 (see V01451) that also includes the SnpR-activated snpA promoter and a modified doxA gene (see V01447) of Streptomyces sp. strain C5. The doxA gene codes for daunomycin C-14 hydroxylase (see W36128), an enzyme capable of converting daunomycin to the anticancer agent doxorubicin. Host cells, especially Streptomyces host cells, transformed with pANT195 can be used in methods for the production of doxorubicin from daunomycin or for the hydroxylation and oxidation of other
                                                                                                                         Producing doxorubicin from daunomycin by daunomycin C14 hydroxylase also hydroxylation and oxidation of other anthracycline(s) with
                                                                                                                                                                                                                  21-MAY-1998 (first entry)
SnpR activator protein.
Daunomycin C-14 hydroxylase; doxA gene; doxorubicin; daunomycin;
13-dihydrocarninomycin; carminomycin; anthracycline;
anticancer; cytostatic; cancer; therapy; plasmid pANT195; SnpR.
Etreptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 85; DB 28; Length 311;
Pred. No. 4.56e+01;
14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                      18..39
/note= "alpha-helix-beta-turn-alpha helix
DNA-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R07143;
24-JAN-1991 (first entry)
Meuronal micotinic acetylcholine receptor beta 4 subunit.
Rat; nAChR.
Rattus rattus.
                                             Score 87; DB 8; Length 343;
Pred. No. 3.27e+01;
13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..20
/label-signal peptide
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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(OHIS ) UNIV OHIO STATE RES FOUND.
DESENTI CL, DICKENS ML, STROH WA;
WPI; 98-018495/02.
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R07143 standard; protein; 495 AA.
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                                                                                                                                                                                      JT 10
W36129 standard; Protein; 311
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Best Local Similarity 33.3%;
Matches 21; Conservative
                                             Query Match 8.9%;
Best Local Similarity 39.0%;
Matches 23; Conservative
 delta subunit holA gene.
                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997.
22-MAY-1997; U08690.
                  343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the same enzyme
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                  Sequence
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ID RC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine adenovirus expression vector system - comprising insertion of required genes into deletions in El and E3 and transformation of mammalian cell lines, useful in vaccines and gene therapy Disclosure; Fig.7H-R; 159pp; English.

BAV3 strain WBR-1 genomic DNA, from between 77 and 92 m.u., was cloned into plasmids and sequenced. ORFs that had the potential to encode polypeptides of at least 50 amino acids (R75756-61) were identified. The amino acid sequence at the N-terminus of the ORF6-encoded protein shared approx. 60% identity with the HAd2 fiber protein tail, but there was little similarity in the knob region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequences for DNA polymerase III holo enzyme sub-units - enzyme with 5 or 6 sub-units having same activity as 10 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 16-17; 115pp; English.
The sequence is that encoded by the DNA polymerase III holoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 983;
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Pred. No. 2.34e+01;
12; Mismatches 15; Indels
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| | |::|::| | | |||:
| 88 LLFQEGGLKLALNGQGLGATSMNQQALEQLRELRIS-GSVQLY 129
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09-DEC-1993; US-164292.
(UYSA-) UNIV SASKATCHEWAN.
Babluk LA, Graham FL, Mittal SK, Prevec L; WPI; 95-22430/29.
N-PSDB; 090769.
            57..259 ...
|abel= N-glycosylation_site
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/label= N-glycosylation_site
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/label= N-glycosylation_site
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/label= N.glycosylation_site
847..849
/label= N.glycosylation_site
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/label- N-glycosylation_site
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/label= N-glycosylation_site
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/label= N-glycosylation_site
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label N-glycosylation_site
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| label = N-glycosylation_site
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R40125;
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Best Local Similarity 32.6%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        New neuronal nicotinic acetyl:choline receptor - compsns. contg.
Thera 4 sub-unit and DNA sequences encoding them.
Sclaim 8: Fig 3; 47pp; English.
Sclaim 8: Fig 3; 47pp; English.
The sequence, of a novel neuronal nicotinic acetylcholine.
The sequence, of a novel neuronal ambda ZAP II prepd.
Therefore at mRNA. The protein subunit can combine with the known subunits, alpha-2,-3, and -4, and beta-2 to form previously unknown functional receptors. The new subunit is expressed in the standard and peripheral nervous systems and in PC12 cells.
It has the characteristics of a ligand gated ion channel subunit, including four transmembrane domains. The cystein residues 128 and 142 of the Torpedo electric organ alpha subint are present at posns. 152 and 166. The beta 4 subunit is distinctive in having four rather than two glycosylation sites. Of the three characteristics of a neuronal beta-type subunits, beta 4 has the logest cytoplasmic
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Pred. No. 4.56e+01;
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Refenemann SF, Deneris ES; Duvoisin RM; Patrick JW; WPI; 90-304987/40.

N-PSDB, Q06068.
                                                          /note="membrane spanning region""
                                                                                           'note="membrane spanning region""
                                                                                                                               'note="membrane spanning region"
                                                                                                                                                               'note="membrane spanning domain"
          21..495
/label=nAChR beta 4 subunit
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/label=N-glycos_site
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Tabel=N-glycos_site
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Cdc2, Gl stage, Gl - S transitic
cancer; interaction trap system
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/label=MSR III
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/label=MSR IV
                                                                               /label=MSR II
                                 237..256
/label=MSR I
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Best Local Similarity 31.9%;
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US-492555.
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20-OCT-1993; U10069.
30-OCT-1992; US-969038.
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14-MAR-1989; 1
12-MAR-1990; 1
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WO9410300-A.
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The second for screening for drugs useful in diagnosis, prognosis and treatment of e.g. neoplasia

Treatment of e.g. neoplasia

Claim 1: Page 25; 32pp: English.

Human signal transducer and activator of transcription 4-beta (W01102) is an interleukin-12 signal transducer protein that binds an intracellular domain of an interleukin-12 protein that binds an intracellular domain of an interleukin-12 receptor subunit. Its amino acid sequence was deduced from a cDNA clone (T38325) isolated from human peripheral blood lymphocytes. A different isoform, Stat4-alpha (W01101), is the produce of a cDNA clone (T38325) obtd. from Jurkat cells. They find use in screening assays for cpds. useful in the diagnosis, prognosis or treatment of diseases associated with undesirable cell growth, sequence 704 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 ltvqssysdghltw-akfckehlpgksftfwt-wleaildlikkhilplwidgyvmgfvs 579
                                                                                                                                                                                                                                                                                                                                The sequence is that of a protein, Cdil, which complexes with Cdc2 family proteins. It is expressed during Gl to S transition and may negatively regulate the passage of cells through this part of the regulatory networks connecting extracellular signals with core cell cycle controls. Cdil may function to remove cells from active cycle to allow differentiation, and there are cancers in which lesions in the Gl regulatory machinary prevent Cdil from exherting its full effect. The protein was isolated using the novel "bait-trap method" described in the specification.
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                                                                                                                                                             Determining whether protein interacts with known protein, esp. with Cdc2 - useful to detect cancer and to develop anticancer
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23.8%; Pred. No. 5.38e+01;
ttive 27; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 8.6%; Score 84; DB 10; Length 212; Local Similarity 45.8%; Pred. No. 5.38e+01; les 11; Conservative 7; Mismatches 6; Indels
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      Gyuris J;
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Best Local Similarity 23.8%;
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22-MAR-1996; U03868.
22-MAR-1995; US-408318.
(TULA-) TULARIK INC.
Golemis E,
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WPI; 96-443132/44.
N-PSDB; T38325.
                                    WPI; 94-167458/20.
N-PSDB; 065494.
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WO9629341-A1.
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                                                                                                                                                                                                                                                                             DNA encoding human signal transducer and activator of transcription of transcription of tractment of e.g. neoplasia tractment of e.g. neoplasia claim 1; Page 21-23; 32pp; English.

Claim 1; Page 21-23; 32pp; English.

Human signal transducer and activator of transcription 4-alpha (Stat4-alpha) (W01101) is an interleukhn-12 signal transducer protein that binds an intracleukhn-12 signal transducer clone (T38324) isolated from a Jurkat cDNA library. A second, truncated isolorm, Stat4-beta (W01102), is the product of a cDNA clone (T38325) obtd. human peripheral blood lymphocytes.

Excombinant Stat4 proteins can be produced in transformed host cells. They find use in screening assays for cpds. useful in the diagnosis, prognosis or treatment of diseases associated with undestrable cell growth, differentiation and/or cytokine signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 ltvqssysdghltw-akfckehlpgksftfwt-wleaildlikkhilplwidgyvmgfvs 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                             Signal transducer and activator of transcription 4-alpha. Signal transducer and activator of transcription 4; Stat4; interleukin-12; signal transduction; neoplasm; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant gene encoding human macrophage carbohydrate - Ige-binding protein and antibody used to treat, diagnose and prevent e.g. inflammatory bowel disorder, leishmaniasis, hayfever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Fig 1; 36pp; English.
Clone Mac2.16 was isolated from a lambda gtl1-P388D1 expression
library prepared from activated mouse macrophages. This is the
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HMEBP; leishmaniasis; Mouse Mac-2; laminin.
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W01101 standard; Protein; 748 AA.
W01101;
03-JAN-1997 (first entry)
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R12531 standard; Protein; 264
R12531;
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109 MNQQALEQLRELRISGSVQL 128
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29-NOV-1999; U5-444195.
14-SEP-1990; U5-444195.
(GEP-) GEN HOSPITAL CORP.
Pillai S, Cherayil BJ;
WPI; 91-193196/26.
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Best Local Similarity 23.8%;
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22-MAR-1996; U03868.
22-MAR-1995; US-408318.
(TULA-) TULARIK INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748 AA;
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WO9629341-A1.
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WO9108290-A.
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195 wg-keerqsafpfesgkpfkiqvlveadhfkvavndahllqynhrmknlreisglgisgd 253
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deduced amino acid sequence of the Mac2.16 expression product. I has predicted mol. wt. 27,482. The N-terminal domain contains a repetitive Proline/Glycine-rich motif and the C-terminal domain contains a sequence found in S-type lectins. See also Q12208-Q12211.
                                                                                                                                   Score 83; DB 3; Length 264;
Pred. No. 6.34e+01;
15; Mismatches 30; Indels
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Local Similarity 27.0%;
nes 17; Conservative
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on:

Tue Dec 15 15:56:27 1998; MasPar time 2.20 Seconds 427.387 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-09-109-864-2 (1-133) from US09109864.pep 980 1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133

PAM 150 Gap 11 Scoring table:

77309 segs, 7078906 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Database:

Mean 28.678; Variance 129.097; scale 0.222 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	BQ.	Q.	Description		Pred. No.
Н	83	9.1	323	7	PCT-US95-0	Sequence 16,	Applicati	1.07e+01
7	83	9.1	323	Н	US-08-469-	Sequence 16,	Applicati	1.07e+01
m	83	9.1	343	Н	US-08-279-	δ	Applicatio	1.07e+01
7	84	8.6	212	П	US-08-461-	35,	Applicati	2.43e+01
Ŋ	84	8.6	748	П	US-08-839-	~	Applicatio	2.43e+01
Ø	84	8.6	748	Н	US-08-408-	7	Applicatio	2.43e+01
7	81	œ . 3	847	-	US-08-781-	7	Applicatio	3.94e+01
∞	81	8.3	847	Ч	US-08-276-	7	Applicatio	3.94e+01
σ	. 80	8.2	785	-	US-08-526-	Sequence 4, 7	Applicatio	4.62e+01
10	79	8.1	227	г	US-08-414-	4	Applicatio	5.42e+01
11	79	8.1	357	7	PCT-US94-0	12,	Applicati	5.42e+01
12	79	8.1	357	٦	US-08-145-	Sequence 12,	Applicati	5.42e+01
13	79	8.1	921	Н	ns-08-396-	Sequence 2, 1	Applicatio	5.42e+01
14	79	8.1	921	Н	US-08-818-	Sequence 2, 1	Applicatio	5.42e+01
12	78	8.0	119	Н	US-08-207-	20,	Applicati	6.35e+01
16	78	8.0	125	Н	US-08-313-	Sequence 54,	Applicati	6.35e+01
17	78		195	7	PCT-US93-0	6	Applicatio	6.35e+01
18	78	8.0	195	Н	us-08-063-	6	Applicatio	6.35e+01
13	78		677	Н	us-08-646-	Sequence 13,	Applicati	6.35e+01
20	78	8.0	677	1	US-08-188-	Sequence 13,	Applicati	6.35e+01
21	77	7.9	312	 1	US-08-414-	7	Applicatio	7.44e+01
22	77	7.9	708	H	US-07-797-	Sequence 2, 1	Applicatio	7.44e+01
23	77	7.9	708	 1	us-08-308-	Sequence 2, 1	Applicatio	7.44e+01

7.44e+01 8.70e+01 8.70e+01 8.70e+01 8.70e+01 8.70e+01 8.70e+01 1.02e+02 1.0					
Application Applic					Proteins Cecchi,
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PCT-US95-0 US-08-162- US-08-485- US-08-485- US-08-036- US-08-036- US-08-036- US-08-781- US-08-781- US-08-450- US-08-450- US-08-450- US-08-450- US-08-450- US-08-451- US-08-451- US-08-431- US-08-335- US-08-335- US-08-335- US-08-335- US-08-335- US-08-335- US-08-335- US-08-341- US-08-341- US-08-341- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278- US-08-278-	ALIGNMENTS	; PRT		PC/TUS9507289	GENERAL INFORMATION: APPLICANT: Yu, Guo-Liang APPLICANT: Tu, Guo-Liang APPLICANT: Rosen, Craig TITLE OF INVENTION: Colon Specific CORRESPONDENCES: 24 CORRESPONDENCES: 24 CORRESPONDENCES: 24 CORRESPONDENCES: Stewart & Oistein STREET: 6 Becker Farm Road CITY: Roseland STATE: NJ COUNTRY: USA ZIP: 07068-1739 COMPUTER: READABLE FORM: MADIUM TYPE: Floppy disk COMPUTER: Patentin Release #1.0, COMPUTER: Patentin Release #1.0, STATE: NJ COMPUTER: Patentin Release #1.0, COMPUTER: Patentin Release #1.0, SOFTWARE: Patentin Release #1.0, COMPUTER: Patentin Release #1.0, SOFTWARE: Patentin Release #1.0, TELECOMPUTER: 101-1994 TELEPATION NUMBER: 325800-; TELECOMMUTCATION NUMBER: 35800-; TELECOMMUTCATION NUMBER: 325800-; TELEFAX: 201-994-1744 INFORMATION FOR EXD ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 323 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein MOLECULE TYPE: protein
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070 070 070 070 084448 0873 0873 0873 0873 0873 0833 0833 083				Application	FORMATION: T: Yu, Guo-Lian T: Yu, Guo-Lian T: Yu, Guo-Lian T: Rosen, Crais E SEQUENCES: 2 SEE: Stewart 6 SEE: S
000000000000000000000000000000000000000		-16		ppl	WIT: YO, SSEE: SI SSE
		-07289		16, A	PELLICANT: YU, G PPLICANT: YU, G ADDRESSEE: Car COUNTRY: NJ COUNTRY: NJ COUNTRY: NJ MEDIUM TYPE: PATE MEDIUM TYPE: PATE SOFTWARRE: PATE OOPERATING SYSTE SOFTWARRE: PATE TILING DATE: OO CLASSIFICATION NUM APPLICATION NUM REFERENCE/DOCKE TILICOMMUNICATION NUM REFERENCE/DOCKE TILICOMMUNICATION TELEPHONE TILICOMMUNICATION TILICOMMUNICA
77 97 97 97 97 97 97 97 97 97 97 97 97 9		1 -0895	XXXXXX	Sequence	Sequence 16, Application PC GENERAL INFORMATION: APPLICANT: TW GUO-Lian APPLICANT: TW GUO-Lian APPLICANT: TW GUO-Lian ITILE OF INVENTION: Col NUMBER OF SEQUENCES: 24 CORESPONDENCE ADDRESS: ADDRESSEE: Stewart & STREET: NJ COUNTRY: NJ COUNTRY: NJ COUNTRY: NJ COUNTRY: NJ COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER TEADABLE FORM: MADESTERM TON NUMBER: TELEPHONE: 201-994-174 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 333 amino acid TYPE: amino acid TYPE: mino acid TYPE: protein SEQUENCE TYPE: protein SEQUENCE TYPE: protein
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63 IS-RWG--QKKLISAPFLEYPQRFFEVLLIFQEGGLKLALNGQGLGATSMNQQALEQLRE 119
                                                                                    192 VPYFGRLQGGLTARRTIIIKGYVPPTGKSFAINFKVGSSGDIALHINPRMGNGTVVRNSL 251
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                                                                                                                Gaps
                                              9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08469667
Patent No. 573348
GENERAL INFORMATION:
APPLICANT: You Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
Score 89; DB 2; Length 323;
Pred. No. 1.07e+01;
36; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/469,667
FILING DATE: 06-JUN-1995
CLASSIFTCATION: 536
ATTORNEY,AGENT INFORMATION:
NAME: FERTATO, GreGOTY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-435
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 323 AA; 35941 MW; 553806 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08469667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: 201-994-1/44
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
  Query Match 9.1%;
Best Local Similarity 24.8%;
Matches 33; Conservative
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ZIP: 07068-1739
                                                                                                                                                                                                                                                            310 LEIQGDVTLSYVQ 322
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C SEQUENCE 16, APPlix

CC SEPERAL INFORMAT: YU

APPLICANT: YU

APPLICANT: YU

APPLICANT: YU

APPLICANT: YU

APPLICANT: YU

CC COUNTRY: CS

CC COUNTRY: CS

CC COUNTRY: US

CC COUNTRY

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Pred. No. 1.07e+01;
14; Mismatches 15; Indels 7; Gaps
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GEORGE M. YANAAK
REGISTRATION NUMBER: 26,824
REGISTRATION NUMBER: 26,824
REERRINGE/DOCKET NUMBER: CRF D-1056CIP
TELECHONE: (203)268-1951
TELEPRA: (203)268-1951
INFORMATION: CO3)268-1951
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08279058B
Patent No. 5668004
GENERAL INFORMATION:
APPLICANT: Michael E. O'Donnell
TITLE OF INVENTION: HOLDENZIME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
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COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: MICROSOft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,058B
                                                                                                                                                                                      PRT;
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SEQUENCE 343 AA; 38674 MW; 551136 CN;
                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08279058B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/08461859
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                                                                                                                                                                                      STANDARD;
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Best Local Similarity 39.0%;
Matches 23; Conservative
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                                                                        310 LEIQGDVTLSYVQ 322
                                                                                                            120 LRISGSVQLYCVH 132
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522 LIVQSSYSDGHLIW-AKFCKEHLPGKSFIFWT-WLEAILDLIKKHILPLWIDGYVMGFVS 579
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Patent No. 5639858
GENERAL INFORMATION:
APPLICANT: Hoey, Timothy
TITLE OF INVENTION: Human Signal Transducers and Binding
TITLE OF INVENTION: Assays
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herber STREET: 850 Hansen Way, #200
STRY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: Flehr, Hobbach, Test, Albritton & Herber STREET: 850 Hansen Way, #200 CITY: Palo Alto STATE: CA STATE: CA COUNTRY: USA ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
8.6%; Score 84; DB 1; Length 748;
Best Local Similarity 23.8%; Pred. No. 2.43e+01;
Matches 19; Conservative 27; Mismatches 30; Indels
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/839,164
FILING DATE: 23-ARR-1997
FLIASSIFICATION: 536
PLIASSIFICATION DATA:
APPLICATION NUMBER: 08/408,318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 748 AA; 85940 MW; 3117180 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMEN RICHARY 36,627
REFERENCE/DOCKET NUMBER: A-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8700
TELEFAX: 415-494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08408318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-494-8771
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTER/STICS:
                                                                                                                                                                                                                                       Floppy disk
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 748 amino acids
TYPE: amino acid
TOPOLOGY: linear
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NUMBER OF SEQUENCES: 4
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MEDIUM TYPE: Floppy of
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US-08-408-318-2
                                                                                                                                                         COUNTRY:
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                                                                                           APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5786169el Proteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Patent No. 5756700
GENERAL INFORMATION:
APPLICANT: Hoey, Timothy
TITLE OF INVENTION: Human Signal Transducers and Binding
TITLE OF INVENTION: Assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 Match 8.6%; Score 84; DB 1; Length 212; Local Similarity 45.8%; Pred. No. 2.43e+01; hes 11; Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                            AUDKESSEE: TISH & ALCHARAUSH F.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordOperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,859
FILING DATE: January 9, 1995
PRIOR APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PRIOR APPLICATION NUMBER: 07/969,038
FILING DATE: January 9, 1995
RILING DATE: October 30, 1992
ATTORNEY AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 00786/143002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 212 AA; 23806 MW; 219064 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                  Sequence 35, Application US/08461859
Patent No. 5786169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08839164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 LSDTISPEQAIDSLRDLRGSGAIQ 181
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104 LGATSMNQQALEQLRELRISGSVQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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US-08-839-164-2
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Matches
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ID US
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4; Gaps

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Sequence 2, Application US/08276099A
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 847 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                 515 W-QWFDGVLDL 524
                                                                                                                                                                                                                                                                                                        79 YPQRFFEVLLL 89
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                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08781890
Patent No. 571026
GENERAL INFORMATION:
APPLICANT: McKnight, Steven L
APPLICANT: McKnight, Steven L
APPLICANT: Hou, Junzhao
TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
TITLE OF INVENTION: BINDING ASSAYS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: San Francisco
STATE: California
COMPUTRY: USA
ZIP: 94111-4187
COMFUTER: LBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: USA/08/781,890
FILING DATE: OS-JAN-1997
CLEING DATE: OS-JAN-1997
                                                                                                                                                                                                                                                                                                          27; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                Query Match 8.6%; Score 84; DB 1; Length 748; Best Local Similarity 23.8%; Pred. No. 2.43e+01; Matches 19; Conservative 27; Mismatches 30; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,318
                                                                                                                                                                                                                                                                                                                                                                                                                                                            847 AA
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APPLICATION NUMBER: US 08/276,099
FILING DATE: 15-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD AFON
                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 748 AA; 85940 MW; 3117180 CN;
                                                                                                                             A-60845
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                          FILING DATE:

ATTORNEY FACENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-608
TELEPHONE: 415-494-8700
TELEPHONE: 415-494-8701
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08781890
                                                                                                                                                                                                                                                                                                                                                                                                 ::: | |::::|: |
109 MNQQALEQLRELRISGSVQL 128
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                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-781-890-2
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                 Query Match
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461 AEVGTNRGL-L--PEHF-LFLAQKIFNDNSLSM-EAFQHRSVSW-SQFNKEILLGRGFTF 514
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Patent No. 5591825
GENERAL INFORMATION:
APPLICANT: MCMIGHT, Steven L
APPLICANT: MCMIGHT, Steven L
APPLICANT: Hou, Jinzhao
TITLE OF INVENTION: INTERLEGINA SIGNAL TRANSDUCERS AND
TITLE OF INVENTION: BINDING ASSAYS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLERK, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.3%; Score 81; DB 1; Length 847; Best Local Similarity 29.6%; Pred. No. 3.94e+01; Matches 21; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: CALLLINING

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,099A

FILING DATE: 15-JUL-1994

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 36,527

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
TELECOMONICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 847 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 847 AA; 94134 MW; 3802900 CN;
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APPLICANT: Goeddel, David V.
APPLICANT: Hsu, Hailing
TITLE OF INVENTION: INTRACELLULAR SIGNALING PROTEINS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79; DB 1; Length 22,,
Pred. No. 5.42e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LQAYREGALRTALQ-RCM-APALAQEALRLQL-ELR-AGAEQL 41
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-60916/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
                                                                                           227
        1 MSPRLEVPCSHALPQGLSPGQV-IIVRGLVLQEPKH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
JENCE 227 AA; 25323 MW; 222467 CN;
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application PC/TUS9400545
                                                                                                                                                                                                                                                       Sequence 4, Application US/08414625
Patent No. 5563039
GENERAL INFORMATION:
                                                                                                                                                                                                                    Sequence 4, Application US/08414625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) ----
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                           STANDARD;
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COMPUTER READABLE FORM:
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Best Local Similarity 41.9%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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PCT-US94-00545-12
                                                                     US-08-414-625-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                             20 GQVIIVRGLVLQEPKHFTVSLRDQA-AHAPVTLRASFADRTLAWISRWGQKKLISAPFLF 78
                                                                                                            8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lambowitz, Alan M
APPLICANT: Zimmerly, Steven
APPLICANT: Zimmerly, Steven
APPLICANT: Yang, Jian
ITILE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold
                                                        Query Match 8 3%; Score 81; DB 1; Length 847; Best Local Similarity 29.6%; Pred. No. 3.94e+01; Matches 21; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.2%; Score 80; DB 1; Length 785; Best Local Similarity 33.3%; Pred. No. 4.62e+01; Matches 12; Conservative 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,964
                                                                                                                                                                                                                                                                                                                                                               785 AA.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 785 amino acids
MOLECULE TYPE: protein
JENCE 847 AA; 94134 MW; 3802900 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        785 AA; 90390 MW; 3218308 CN;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08526964
Patent No. 5698421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08526964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: GOLFICK, MARY E
REGISTRATION NUMBER: 34,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 800 Superior Avenue CITY: Cleveland STATE: Ohio COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
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79 YPQRFFEVLLL 89
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ID US-08-526-964-4
                       SEQUENCE
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Patent No. 5612455
GENERAL INFORMATION:
APPLICANT: HOEY, Timothy
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEBRA, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STREET: California
COUMTRY: USA
ZIP: 94111
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                             AUNKESSEE: E.C. E.C. CITY: Boston
STATE: Boston
STATE: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02.10-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,006C
FILING DATE: Cottober 29, 1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/017,052
FILING DATE: FEDRUARY 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: FEDRUARY 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: FADRUARY 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: FADRUARY 11, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 04590/007001
TELEPRONE: (617) 542-8906
TELEPRONE: (617) 542-8906
TELERA: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            921 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSPRLEVPCSHALPQGLSPGQVIIVRGLVLQEP 33
                                  E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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ICE 357 AA; 37623 MW; 700002 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08396479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-396-479B-2
                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
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APPLICANT: Hogan, Patrick Gerald
APPLICANT: McCaffrey, Patricia
APPLICANT: Jain, Jugar, Patricia
APPLICANT: Jain, Jugar
TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE
TITLE OF INVENTION: DNA-BINDING PROTEIN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08145006C
Patent No. 5656452
GENERAL INFORMATION:
APPLICANT: Rao, Anjana
APPLICANT: Hogan, Patrick Gerald
APPLICANT: McCaffrey, Patricia
APPLICANT: Jain, Jugnu
TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE
TITLE OF INVENTION: DNA-BINDING PROTEIN
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                   STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTR: U.S.A.
ZIP: 0210-2804
COMPUTR: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: MondDerfect (Version 5.1)
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00545
FILING DATE: 18-JAN-1994
CLASSIFICATION NUMBER: 08/017,052
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/017,052
FILING DATE: GAINER: 08/010,057
FILING DATE: GAINER: 08/010,057
FILING DATE: GAINER: 08/010,07001
FELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELEPHARICHUR FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 AA.
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1 MSPRLEVPCSHALPQGLSPGQVIIVRGLVLQEP 33
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357 AA; 37623 MW; 700002 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08145006C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
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XX
AC XXXXXX
XX
XX
XX
DT
XX
DE Sequence 12, Applic
XX
C Sequence 12, Applic
C Patent No. 5656452
CC APPLICANT: Rao
CC APPLICANT: Hog
CC APPLICANT: Hog
CC APPLICANT: Hog
CC APPLICANT: Jai
CC APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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Gaps
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8.0%; Score 78; DB 1; Length 119;
Best Local Similarity 28.3%; Pred. No. 6.35e+01;
Matches . 15; Conservative 17; Mismatches 17; Indels
                                                                                                                                                  Length 921;
                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08207996
Patent No. 564623
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: 1014 Hamilton Court
APPLICANT: 1014 Avenue of the America
APPLICANT: 1345 Avenue of the America
APPLICANT: United States of America
APPLICANT: United States of America
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OURTOLIES. THE TO COMPOSE TO COMP
                                                                                                                                                                                                                                                                                                                                                                                               119 AA
                                                                                                                                                Score 79; DB 1; I
Pred. No. 5.42e+01;
                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                            109 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 140
                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 921 AA; 99784 MW; 4492223 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ENCE 119 AA; 12852 MW; 80291 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08207996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
  LENGTH: 921 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                             Query Match 8.1%;
Best Local Similarity 36.4%;
Matches 12; Conservative
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US-08-207-996-20
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Fatent No. 5708158
GENERAL INFORMATION:
APPLICANT: HOEY, Timothy
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING ASSAY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.1%; Score 79; DB 1; Length 921; Best Local Similarity 36.4%; Pred. No. 5.42e+01; Matches 12; Conservative 12; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,823
FILING DATE: 14 MAR-1997
CLASSIFICATION: 536
                        FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
RAGISTRANION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59450-1/RAO
TELECHONE: (415) 494-8770
TELERAX: (415) 494-8771
TELEX: 210 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                921 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LSPRIEITPSHELIQAVGPLRMRDA-GLLVEQP 140
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,479B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 921 AA; 99784 MW; 4492223 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/396,479
FILING DATE: 02-MAR-1995
ATTONBE/AGENT INFORMATION:
NAME: OSMBAN, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08818823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 494-8771
TELEX: 210 277299
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JT 14
US-08-818-823-2
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Search completed: Tue Dec 15 15:56:35 1998 Job time : 8 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Tue Dec 15 15:54:30 1998; MasPar time 7.48 Seconds 606.724 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

>US-09-109-864-2 (1-133) from US09109864.pep 980 1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

107076 seqs, 34141958 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 42.737; Variance 90.659; scale 0.471 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7.78e-12	1.19e-06	4.56e-06	9.92e-03	2.46e-02	2.46e-02	6.03e-02	4.60e-01	6.11e-01	1.41e+00	1.41e+00	2.45e+00	2.45e+00	3.22e+00	3.22e+00	4.21e+00	5.50e+00	5.50e+00	5.50e+00	7.18e+00	7.18e+00	7.18e+00	9.34e+00
galectin-5 - rat	prostate carcinoma tu	galectin-7 - human	beta-galactoside-bind	galectin-8 - rat	Jactose-binding lecti	UDP-N-acetylglucosami	14K beta-galactoside-	nosF protein - Pseudo	enterobactin receptor	sodium channel protei	probable general secr	sodium channel protei	complement factor I (glutathione-regulated	ATP-binding cassette	galactoside-binding p	multidrug resistance	pqqF protein - Klebsi	global nitrogen regul	hetical 87.1K	(EC 1.	virC-region hypotheti
A55932	JC6147	155469	A42846	A55975	A46631	A27522	LNCH14	S13584	A40636	A60165	A65126	JC1101	A29154	QQECRD	B41538	A49800	A64101	S20458	A48640	JQ1866	S57964	B40361
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145	317	136	279	316	324	448	135	308	746	1321	493	1522	583	620	703	242	510	761	225	833	862	137
17.8	14.3	13.9	11.4	11.1	11.1	10.8	10.1	10.0	9.7	7.6	9.5	9.5	9.4	9.4	9.3	9.5	9.5	9.5	9.1	9.1	9.1	0.6
174	140	136	112	109	109	106	66	86	95	95	93	66	92	92	91	90	90	90	86	88	83	88
-	7	m	4	S	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23
	2 galectin-5 - rat 7	17.8 145 2 A55932 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1.	17.8 145 2 A55932 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1.3.9 136 2 155469 galectin-7 - human 4.	17.8 145 2 A55932 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.4 279 2 A42846 beta-qalactoside-bind 9.	17.8 145 2 A55932 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.4 279 2 A42846 beta-qalactoside-bind 9. 11.1 316 2 A55975 galectin-8 - rat 2.	17.8 145 2 A55332 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.4 279 2 A42846 beta-galactoside-bind 9. 11.1 324 2 A55575 galectin-8 - rat 2. 11.1 324 2 A46631 lactose-binding lecti 2.	17.8 145 2 A55332 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.4 279 2 A42846 beta-galactoside-bind 9. 11.1 316 2 A55975 galectin-8 - rat 2. 11.1 314 2 A46531 lactose-binding lecti 2. 10.8 448 2 A27522 UDP-N-acety/glucosami 6.	17.8 145 2 A55932 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.1 316 2 A42846 beta-galactoside-bind 9. 11.1 316 2 A55975 galectin-8 - rat 2. 11.1 324 2 A46631 lactose-binding lecti 2. 10.8 448 2 A27522 UDP-N-acetylglucosami 6. 10.1 135 1 LNCH14 14K beta-galactoside 4.	17.8 145 2 A55932 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.1 316 2 A42846 beta-galactoside-bind 9. 11.1 324 2 A45875 galectin-8 - rat 2. 11.1 324 2 A46631 lactose-binding lecti 2. 10.8 448 2 A27522 UDP-N-acetylglucosami 6. 10.1 135 1 LNCH14 14K beta-galactoside-4. 10.0 308 2 S13584 nosf protein - Pseudo 6.	17.8 145 2 A55332 galectin-5 - rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 155469 galectin-7 - human 4. 11.4 279 2 A42846 beta-galactoside-bind 9. 11.1 324 2 A45575 galectin-8 - rat 2. 11.1 324 2 A45575 galectin-8 - rat 2. 11.1 324 2 A45631 lactose-binding lecti 2. 10.8 448 2 A27522 UDP-N-acetylglucosami 6. 10.1 135 1 LNCH14 14K beta-galactoside- 4. 10.0 308 2 513584 nosF protein - Pseudo 6. 9.7 746 2 A40636 enterobactin receptor 1.	17.8 145 2 A55922 galectin-5 rat 7. 14.3 317 2 JC6147 prostate carcinoma tu 1. 13.9 136 2 A52846 galectin-7 human 4. 11.1 316 2 A55975 galectin-8 rat 2. 11.1 324 2 A46631 lactose-binding lecti 2. 11.1 324 2 A46631 lactose-binding lecti 2. 10.8 448 2 A27522 UDP-N-acetylglucosami 10.1 135 1 LNCH14 14K beta-galactoside 4. 10.0 308 2 S13584 nosF protein - Pseudo 6. 9.7 136 2 A40636 sodium channel protei 1.	17.8 145 2 A55932 galectin-5 - rat 14.3 317 2 JC6147 prostate carcinoma tu 1.3.9 136 2 155469 galectin-7 - human 4.11.1 316 2 A42846 beta-galactoside-bind 9.11.1 324 2 A46631 lactose-binding lecti 2.10.8 448 2 A27522 UD-N-acetylglucosami 6.10.1 135 1 LNCH14 14K beta-galactoside-4.10.0 308 2 S13584 nosF protein - Pseudo 6.9.7 1321 2 A40636 enterobactin receptor 1.9.7 1321 2 A60165 probable general secr. 2.9.5 493 2 A65126 probable general secr. 2.	17.8 145 2 A55932 galectin-5 - rat 14.3 317 2 JC6147 prostate carcinoma tu 1.3.9 136 2 155469 galectin-7 - human 4.11.1 316 2 A55975 galectin-8 - rat 11.1 324 2 A46631 lactose-binding lecti 2.11.1 324 2 A46631 lactose-binding lecti 2.10.8 448 2 A27522 UDP-N-acetylglucosami 6.10.1 135 1 LNCH14 lack beta-galactoside-4.10.0 308 2 S1384 nosf protein - Pseudo 6.9.7 1321 2 A60165 sodium channel protei 1.9.7 1321 2 A65126 probable general secr 2.9.5 493 2 JC61101 sodium channel protei 2.	174 17.8 145 2 A55932 galectin-5 rat 140 14.3 317 2 UCG147 prostate carcinoma tu 136 13.9 136 2 155469 galectin-7 human 4.109 11.1 316 2 A458975 galectin-8 rat 109 11.1 324 2 A458975 galectin-8 rat 109 11.1 324 2 A45631 lactose-binding lecti 2 106 10.8 448 2 A45531 lactose-binding lecti 2 106 10.8 448 2 A457522 UDP-N-acety/glucosami 6 99 10.0 308 2 51384 nosF protein receptor 195 9.7 746 2 A46336 enterobactin receptor 195 9.7 1221 2 A60165 sodium channel protei 193 9.5 1522 2 UCII01 sodium channel protei 2 92 9.4 583 2 A29154 complement factor I (3.2)	174 17.8 145 2 A55332 galectin-5 - 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##residues 1-317 ##label SUA
##cross-references GB:L7813; NID:91932711; PID:91932712
## This protein is a therapeutic reagent for intervention in pervasive
TT is protein is a therapeutic reagent for intervention in pervasive
and fatal neoplastic disease. It is involved in an earlier
genetic change in human prostate cancer development. This protein
is a member of the gelectin familly.
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Surface-epitope masking and expression cloning identifies the
human prostate carcinoma tumor antigen gene PCTA-1 a member
of the galectin gene family.
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J. Biol. Chem. (1995) 270:5823-5829
Cloning, expression, and chromosome mapping of human
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70 NTQINNSWGPEERSLPGSMPFSRGQRF-SVWILCEGHCFKVAVDGQHICEYSHRLMNLPD 128
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#formal_name Homo sapiens #common_name man
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Su, Z.Z.; Lin, J.; Shen, R.; Fisher, P.E.; Goldstein,
Fisher, P.B.
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J. Biol. Chem. (1992) 267:15485-15490
Evidence that Caenorhabditis elegans 32-kDa
beta-galactoside-binding protein is homologous to
vertebrate beta-galactoside-binding lectins. cDNA cloning
and deduced amino acid sequence.
                                                                                                                                              63 NSKEQGSWGREERGPGVPFQR-GQPF-EVLIIASDDGFK-AVVGDAQYHHFRHRLPLARV 119
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beta-galactoside-binding protein GBP - Caenorhabditis el

beta-galactoside-binding lectin homolog, 32K

#formal_name Caenorhabditis elegans

10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
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10-Sep-1997
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Galectin-8. A new rat lectin, related to galectin-4.
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41; Mismatches 58; Indels
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12; Mismatches 13;
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Pred. No. 4.56e-06;
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#accession A42846
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Best Local Similarity 35.9%;
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Best Local Similarity 22.1%;
Matches 30; Conservative
Query Match 13.9%;
Best Local Similarity 28.1%;
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                                     38; Conservative
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N-acety1glucosaminephosphotransferase (EC 2.7.8.15) - yeast
(Saccharomyces cerevisiae)
protein YBR1628; protein YBR243c
#formal_name Saccharomyces cerevisiae
15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
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J. Biol. Chem. (1993) 268:5929-55939
Soluble lactose-binding lectin from rat intestine with two different carbohydrate-binding domains in the same peptide
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Purification and characterization of the N-terminal domain galectin-4 from rat small intestine.
S69096
HLSLPFEARLNASMGPGRTVVVKGEVNTNATSFNVDLVAGRSRDIALHLNPRLNVKAFVR 240
                                                                 241 NSFLQDAWGEEERNITCFPFSSGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKD-LSSI 299
                                                                                  63 IS--R--WGQKKLISAPFLEYPQRFFEVLLLFQEGGLKLALNG-QGLGATSMNQQALEQL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence extracted from NCBI backbone (NCBIN:128409, NCBIP:128410)
                   #formal_name Rattus norvegicus #common_name Norway rat
21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998
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##experimental_source intestine
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##residues 13-37;44-50,'E',52-66 ##label TAR
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                                                                                                                                                                                                                                                       lactose-binding lectin L-36 - rat
                                                                                                                                                                                                                                           #type complete
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##molecule_type nucleic acid
##residues 1-324 ##label ODA
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#cross-references MUID:93194902
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A46631
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les 31; Conservative
                                                                                                                                   300 DTLAVDGDIRLLDVRS 315
                                                                                                                                                                   118 RELRISGSVQLYCVHS 133
                                                                                                                                                                                                                                                                       galectin-4
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122 ISGSVQLYCVH 132
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13-Mar-1998
A2752; S46120
RERENCE A2752
#authors Hartog, K.O.; Bishop, B.
#journal Nucleic Acids Res. (1987) 15:3627
#title Genomic sequence coding for tunycamicin resistance in yeast.
#accession A27522
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14K beta-galactoside-binding lectin - chicken
14K lectin
14K lectin
31.Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aljinovic, G.; Pohl, F.M.; Pohl, T.M. submitted to the Protein Sequence Database, August 1994 846120
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J. Biochem. (1987) 101:775-783
Complete amino acid sequence of 14 kDa
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#journal J. Biochem. (1988) 104:173-177
#title Isolation and characterization of the chick 14K
beta-galactoside-binding lectin gene.
#cross-references MUID:89033999
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Pred. No. 6.03e-02;
21; Mismatches 32; Indels
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##cross-references EMBL:Y00126; NID:94684; PID:94685
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Best Local Similarity 24.7%;
Matches 19; Conservative
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#title

KEYWORDS 2-135

FEATURE

GENETICS

REFERENCE

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80K - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                           ##status preliminary
##molecule_type nucleic acid
##residues 1-746 ##label DEA
##cross-references GB:M98033; NID:g151434; PID:g151435
##note extracted from NCBI backbone (NCBIN:122308,
NCBIP:122309)
                      A40636 #type complete enterobactin receptor protein, 80K - Pseudomonas aerugin enterobactin receptor protein, 80K - Pseudomonas aeruginosa 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998 A40636 A40636
                                                                                                                                                                        #authors Dean, C.R.; Poole, K. #journal J. Bacteriol. (1993) 175:317-324 Cloning and characterization of the ferric enterobactin receptor gene (pfeA) of Pseudomonas aeruginosa. #cross-references MUID:931213148
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Pred. No. 1.41e+00;
10; Mismatches 12; Indels
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#length 746 #molecular-weight 80967 #.
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Best Local Similarity 37.8%;
Matches 14; Conservative
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S04029
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#journal Bur. J. Biochem. (1990) 192:391-599
#title Bur. J. Biochem. (1900) 192:391-599
#title Stutzeri. Genes for copper-processing and properties of the deduced products, including a new member of the family of #TP/GTP-binding proteins.
                                                                                                                                     S.; Kawasaki, H.;
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                                                                                                                                Ohyama, Y.; Hirabayashi, J.; Oda, Y.; Ohno, S.; Kawasaki, Suzuki, K.; Kasal, K.
Bucchem. Blophys. Commun. (1986) 134:51-56
Nucleotide sequence of chick 14K beta-galactoside-binding
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nosF protein - Pseudomonas stutzeri
#formal_name Pseudomonas stutzeri
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
20-Feb-1998
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experimental #label MAT\
#modified_site acetylated amino end (Ser) (in mat
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#length 135 #molecular-weight 15063 #checksum 8342
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#length 308 #molecular-weight 33777 #checksum 7279
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beta-galactoside-binding lectin of chick embryo.
#cross-references MUID:87250364
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acetylated amino end; lectin
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Pred. No. 4.60e-01;
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                                                            ##molecule_type protein
##residues 2-110,112-135 ##label
ENCE A24062
                                                                                                                                                                                                                                                                                                       12-135 ##label OH2
                                                                                                                                                                                                                     lectin mRNA.
#cross-references MUID:86130505
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Local Similarity 27.9%;
nes 12; Conservative
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#authors Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.
#journal Nucleic Acids Res. (1987) 15.8569-8572
#title Nucleotide sequence of the putative sodium channel gene from Drosophila: the four homologous domains.
#cross-references MUD:88040482
A60165 #type fragments
sodium channel protein – fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing
                                                                                                                                              (fragments)
#formal_name Drosophila melanogaster
22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
16-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1321;
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237,72; 316/7; 362/3; 414/3; 471/2; 531/3;
htrons 751/2; 801/1; 908/1; 960/3; 1005/1
XY #length 1321 #checksum 3413
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##molecule_type DNA
##molecule_type DNA
1-362;363-626;627-1321 ##label SAL
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##molecule_type protein
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Biochem. Biophys. Res. Commun. (1992) 186:61-68
Primary structure of squid sodium channel deduced from the

    Escherichia

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#formal_name Loligo bleekeri #common_name Bleeker's squid
09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
20 Mar-1998
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##cross-references GB:D14525; NID:g1003908; PID:g287449
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#domain transmembrane #status predicted #label TM2\
                        Gaps
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#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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   The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
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-#length 493 #molecular-weight 54610 #checksum 4544
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probable general secretion pathway protein e
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Pred. No. 2.45e+00;
15; Mismatches 28; Indels
  Pred. No. 1.41e+00;
13; Mismatches 14; Indels
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                                                            736 SLRTLRALRPLRAISRWQGMRIVVNALMYAIPSIFNVLLV 775
                                                                                                   50 TLRASFADRTLAWISRWGOKKLISAPFLFYPORFFEVLLL 89
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Best Local Similarity 31.9%;
Matches 22; Conservative
Local Similarity 32.5%;
nes 13; Conservative
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V.C., Perkins, S.J.
FEBS Lett. (1995) 371:199-203
beta-Sheet secondary structure of an LDL receptor domain from complement factor I by consensus structure predictions and
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structure and assignment of its gene to chromosome
#cross-references MUID:87280021
#accession A28434
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complement factor I (EC 3.4.21.45) precursor - human
C3b/C4b inactivator
#formal_name Homo sapiens #common_name man
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_char
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Goldberger, G.; Bruns, G.A.P.; Rits, M.; Edge, M.D.;
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#domain transmembrane #status predicted #label
#domain transmembrane #status predicted #label
#length 1522 #molecular-weight 174113 #checksum 27
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12; Mismatches 14; Indels
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##residues 1-557,'F',559-583 ##label GOL
##cross-references GB:J02770; NID:g182606; PID:g182607
SNCE S66420
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Characterization of the primary amino
complement control protein factor I
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J. Biol. Chem. (1987) 262:10065-10071
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                                                         transmembrane
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##residues 1-583 ##label CAT
##cross-references GB:Y00318
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ecross references MUID:87241401
facession A29154
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Best Local Similarity 35.0%;
Matches 14; Conservative
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#journal Nucleic Acids Res. (1980) 8:2255-2274
#title Nuclections sequence of the Escherichia coli gene coding for dibydrocolate reductase.
#cross-references MUID:81053692
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glutathione-regulated potassium efflux system protein kefc
Escherichia coli
#formal_name Bscherichia coli
65-Apr.-1983 #sequence_revision 01-Mar-1996 #text_change
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                                                                                                                                                                     #superfamily LDL receptor ligand-binding repeat homology;
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#title The cloning and DNA sequence of the gene for the glutathione-regulated potassium-efflux system KefC Escherichia coli.
#cross-reference MUID:91260444
#accession S15165
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#length 583 #molecular-weight 65720 #checksum 3015
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3; Mismatches 7; Indels
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##cross-references EMBL:X56742; NID:g41874; PID:g41875
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                                                               ane GDB:IF
##cross-references GDB:120077; OMIM:217030
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##residues 500-620 ##label SMI
258-269 ##label ULI
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Best Local Similarity 52.4%;
Matches 11; Conservative
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CLASSIFICATION #superfam
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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CLASSIFICATION #superfamily glutathione-regulated potassium efflux system
protein kefC
KEYWORDS potassium transport; transmembrane protein
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#domain transmembrane #status predicted #label TM2\
#domain transmembrane #status predicted #label TM3\
#domain transmembrane #status predicted #label TM4\
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#domain transmembrane #status predicted #label TM5\
#domain transmembrane #status predicted #label TM6\
#domain transmembrane #status predicted #label TM6\
#length 620 #molecular-weight 67795 #checksum 3086
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#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
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Pred. No. 3.22e+00;
19; Mismatches 27; Indels 10;
                                                                                                                                                                                                                                                                                                                     preliminary; nucleic acid sequence not shown; translation not shown
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Job time: 23 secs.
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Best Local Similarity 34.9%;
Matches 30; Conservative
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protein - protein database search, using Smith-Waterman algorithm Tue Dec 15 15:55:45 1998; MasPar time 10.89 Seconds 608.412 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-09-109-864-2 (1-133) from US09109864.pep 980

1 MSPRLEVPCSHALPQGLSPG......LEQLRELRISGSVQLYCVHS 133

PAM 150 Gap 11 Scoring table:

165420 seqs, 49795644 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb16 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_huvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 42.859; Variance 78.955; scale 0.543 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	6.48e-09	4.56e-08	1.46e-03	2.07e-03	2.93e-03	2.93e-03	4.14e-03	3.18e-02	6.19e-02	8.61e-02	1.19e-01	2.28e-01	2.28e-01	3.15e-01	4.33e-01	5.95e-01	5.95e-01	8.15e-01	1.52e+00	1.520+00
	Description	36 KD BETA-GALACTOSIDE	GALECTIN-8.	GALECTIN-7.	W09H1.6B.	GALECTIN-3.	GALECTIN-6.	GALECTIN.	F52H3.7.	BETA-GALACTOSIDE-BINDI	GALECTIN-7.	BETA-A PROTEIN.	TERPENE CYCLASE LIKE P	COMPLEMENT COMPONENT F	REVERSE TRANSCRIPTASE.	PUTATIVE INNER MEMBRAN	ABC-TRANSPORTER.	SODIUM CHANNEL PROTEIN	GALECTIN.	HYPOTHETICAL 19.2 KD P	GALECTIN
	ឧ	035866	015215	054974	045904	090713	054891	044126	020684	025597	054958	083076	065434	061129	064428	070110	028438	027930	001411	066441	001410
	DB	11	4	11	'n	13	11	Ŋ	ഹ	Ŋ	11	14	10	11	10	~	Φ.	Ŋ	Ŋ	~	'n
	Query Match Length DB	354	318	136	285	262	301	283	1262	280	132	195	573	603	1309	295	703	1320	278	166	278
p	Query	14.9	14.4	11.5	11.4	11.3	11.3	11.2	10.6	10.4	10.3	10.2	10.0	10.0	6. 6.	8.6	9.7	7.6	9.6	4.6	4.6
	Score	146	141	113	112	111	111	110	104	102	101	100	86	86	97	96	95	95	94	92	92
	Result No.	П	7	m	7	'n	9	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20

CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)

318 AA.

PRT;

ULT 2 015215 PRELIMINARY; 015215 01-JAN-1998 (TREMBLREL. 05, CF 01-JAN-1998 (TREMBLREL. 05, LA

RESULT ID OLD AC OLD DT OLD DT OLD

: | ::| :| |:: 117 LRELRISGSVQLYCVHS 133

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11.5226 11.5226 12.5226 13.	9.24e+00 9.24e+00 9.24e+00 9.24e+00
· · · · 🖭 · · · · · · · · · · · · · · ·	PLASMID PRJ1004 DNA. CTTOCHROME OXIDASE SUB 403AA LONG HYPOTHETICA RECEPTOR-LIKE PROTEIN HYPOTHETICAL 77.8 KD P
028435 028436 0528436 053840 0172840 0172840 007208 007208 007208 007625 007625 007625 007769 005769 005769 005769 005769	047455 047472 058825 064397 067400
9992574 971 11 11 12 2	70187
703 703 703 2124 250 828 828 839 8424 198 8424 198 198 198 198 198 198 198 198 198 198	309 353 403 642 682
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9922 9922 9922 9932 9932 9932 9932 9932	88888 88888
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                                                                                                                                                                                                                                            181 TPQLRLPFAARLNTPMGPGRTVVVKGEVNANAKSFNVDLLAGKSKDIALHLNPRLNIKAF 240
                                                                                                                                                                                                                                241 VRNSFLØESWGEEERNITSFPFSPGMYFEMIIYCDVREFKVAVNGVHSLEYKHRFKE-LS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 KWGREERGIGIPFQR-GQPF-EVLLIATEEGFK-AVVGDD-EYLHFHHRLPPARVRLVEV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 SLPQGVRVGTVMRIRGLVPDQAGRFHVNLLCGEEQGADAALHFNPRLDTSEVVFNTKQQG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                       Gaps
                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 136;
                                                                                                                                                    Length 318;
                                                                                                                                                                     41; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C59 BLACKC/6;
MAGNALDO T., FOWLIS D., DARMON M.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF038562; G2708654; --
EMBL; AF03809; LECTIN_GALACTOSIDE; 1.
SEQUENCE 136 AA; 15173 MW; 61A0164B CRC32;
                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.5%; Score 113; DB 11; L
Best Local Similarity 27.7%; Pred. No. 1.46e-03;
Matches 36; Conservative 37; Mismatches 44;
                                                      SEQUENCE FROM N.A.
TISSUE-BRAIN HIPPOCAMPUS;
HADARI Y.R., EISENTEIN M., ZAKUT R., ZICK Y.;
TRENDS GLYCOSCI. GLYCOTECHNOL. 9:103-112(1997).
EMBL: X91790; E199407;
EMBL: PS003309; LECTIN_GALACTOSIDE; 1.
PROSITE; PS003307; Gal.blind_lectin.
SEQUENCE 318 AA; 35864 MW; 8FID554C CRC32;
                                                                                                                                                            Pred. No. 4.56e-08;
                                                                                                                                                   DB 4;
                                                                                                                                                   Score 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C59 BLACKC/6;
MEDLINE; 95246905.
MAGNALDO T., BERNERD F., DARMON M.:
DEV. BIOL. 168:259-271(1995).
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                     ULT 3
054974
054974
01-3071-1998 (TREMBLREL. 06, CF
01-3071-1998 (TREMBLREL. 06, LA
01-3071-1998 (TREMBLREL. 06, LA
                                                                                                                                                                                                                                                                                   : | |:| ::| |:|
116 QLRELRISGSVQLYCVHS 133
                                                                                                                                                  Match 14.4%;
Local Similarity 24.6%;
les 34; Conservative
                                                                                                                                                                                                                                                                     300 SIDTLEINGDIHLLEVRS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| ||| ::
SGSVQLYCVH 132
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GALECTIN-8.
                                                                                                                                                   Query Match
                                                                                                                                                                      Matches
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THE SEQUENCE FROM N.A.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., WILSON R., AINSCOUGH R., ANDERSON K., COLLSON R., CRAXTON M., BURTON J., CONNELL M., COPER J., COULSON R., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., RA HAWKINS T., HILLER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMITRARAY A., MORTINARE D., SAUNDERS D., SHOWNKERN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WALESTON J., THIERRY-MIEG J., THOMAS K., WILKINSON-SPROAT J., WOHLDMAN P.;

RA WILKINSON-SPROAT J., WOHLDMAN P.;

RA WILKINSON-SPROAT J., WOHLDMAN P.;

RA MILKINSON-SPROAT J., WOHLDMAN P.;

BURDIS 282081; E1247370; -.

DR PROSITE; PS00309; LECTIN_GALACTOSIDE; 2.

SEQUENCE 285 AA; 32683 MW; 920E5744 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AAPLKVPYDLPLPAGLMPRLLITITGTVNSNPNRFSLDFKRGODIAFHFNPRFKEDHKRV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 IVCNSMFQNNWGKEERTAPRFFFEPGTPFKLQVLCEGDHFKVAVNDAHLLQFNFREKKLN 24.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                 IUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                            SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.07e-03;
12; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111; DB 13;
Pred. No. 2.93e-03;
30; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 VPYRSVLQEKFEPGQTLIVKGSTIDESQRFTINLHSKTA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LECTIN.
SEQUENCE 262 AA; 28155 MW; FD6F1E17 CRC32;
                     285 AA.
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-CARTILAGE;
NURMINSKAYA M.V., LINSENMAYER T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEV. DYN. 0:0-0(0).
EMBL, U50339; G1389600; -.
PFAM; PF00337; Gal-bind_lectin.
                                                                06,
06,
07,
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Best Local Similarity 25.0%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.4%;
Best Local Similarity 35.9%;
Matches 14; Conservative
1LT 4 PRELIMINARY;
045904 O45904 O15904 O1-JUN-1998 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. 0
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                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
                                                                                                                                                           CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Q90713
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Query Match
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Q20684
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Matches
                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 LPYVGALQGGFTVRRTIIIKGYVLPTAKTFAINFRVGSSEDIALHINPRIGDCLVRNSYM 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 NGSWGTEERMVAYN-PFGPGQFFDLSIRCGMDRFKVFANGIHLFNFSHRFQALRKINTLE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 S-RWG-QKKLISAPFLFYPQRFFEVLLLFQEGGLKLALNGOGLGATSMNOQALEOLRELR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; SPIRURIDA
                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GITT M.A., XIA Y.R., ATCHISON R.E., LUSIS A.J., BARONDES S.H.
LEFFLER H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 301;
                                                                                                                                                                                                                                                                                                                                             GITT M.A., COLNOT C., POIRIER F., NANI K.J., BARONDES S.H.
LEFFLER H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110; DB 5; Length 283;
Pred. No. 4.14e-03;
12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEWLANDS G.F.J., SKUCE P.J.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF036098; G2687413; -.
PROSITE: PS00309; LECTIN GALACTOSIDE; 2.
SEQUENCE 283 AA; 32530 MW; 9EAE3746 CRC32;
                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 111; DB 11;
Pred. No. 2.93e-03;
36; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. BIOL. CHEM. 273:2961-2970(1998).
EMBL; AF026799; G2914749; -.
EMBL; AF026796; G2914749; JOINED.
EMBL; AF026798; G2914749; JOINED.
EMBL; AF026798; G2914749; JOINED.
SEQUENCE 301 AA; 34112 MW; 7C5AF97F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 AA
                                                                                            301 AA
                                                                                                                                  CREATED)
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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06,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%;
25.2%;
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06,
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Best Local Similarity 35.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                BIOL. CHEM. 0:0-0(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 25.2%;
hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                044126 PRELIMINARY;
044126;
04-01-1098 (TREMBLREL. 06
01-JUN-1998 (TREMBLREL. 06
01-AUG-1998 (TREMBLREL. 06
: | |:| : | |
116 QLRELRISGSVQLYCV 131
                                                                                            PRELIMINARY;
                                                                                                                              01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAEMONCHUS CONTORTUS.
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122 ISGSVQLYCVH 132
                                                                                                                                                                                                                                                                  EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SV;
MEDLINE; 98112848.
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                                                                                                                                                                                                                                                                                                                         STRAIN=129/SV
                                                                                                                                                                                       GALECTIN-6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                            054891;
                                                                        T 6
054891
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Matches
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RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., WILSON R., AINSCOUGH R., ANDERSON K., COMPER J., CONNELL M., COPER J., COURED, M., CRAXTON M., BARNIN J., LAISTEN J., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., RA HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., A MCMURARY A., MONTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RA MCMURAY A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THERRY-MIEG J., THOMAS K., A WILKINSON-SPROAT J., WOHLDMAN P., RA WILKINSON-SPROAT J., WOHLDMAN P., RESERVED J., WOHLDMAN P., BREEN J., WOHLDMAN P., SHOWS J., WEINSTOCK L., THOMES 368:32-38(1994).

BR FEMBL: 266512; G1041326; -.

DR PFAM; PF00337; Gal-bind_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1132 VPYESGLAGEGLAPGKTLTVFGIPEKKAKRFHINLLKKNGDIALHLNARFDEKHVVRNS 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                GARDNER A.;
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                       Score 104; DB 5;
Pred. No. 3.18e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VPYRSKLTESFEPGQTLLVKGKTAEDSVRFTINLHNTSA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102; DB 5;
Pred. No. 6.19e-02;
15; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 AA; 31978 MW; FC532581 CRC32;
15 VPYRSLLQEKIEPGQTLIVKGSTIDESQRFTINLHSKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                     1262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 95059219.
KIJON A.D., DONELSON J.E.;
MOL. BIOCHEM. PARASITOL. 65:305-315(1994).
EMBL; U04046; G433317; -.
PFAM; PF00337; Gal-bind_lectin.
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-GALACTOSIDE-BINDING LECTIN. ONCHOCERCA VOLVULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.4%; silarity 30.8%; E
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01,
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|larity 27.1%;
|Conservative
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                (TREMBLREL.
                                                                                                                                                                                                                            L-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS
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Best Local Similarity 2
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nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                             01-NOV-1996
01-NOV-1996
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SEQUENCE FROM N.A.
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064428
064428;
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261129
261129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PLPQGVRLGTVMRIRGVVPDQAGRFHVNLLCGEEQEADAALHFNPRLDTSEVVFNTKQQG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYCHNIS RINGSPOT VIRUS.
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; ROD-SHAPED SS-RNA VIRUSES;
HORDEIVIRUS.
                                                                                                                                           RATIUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 11;
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EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 PSNALVARDVQPLRDSALHFTYDLKDLVTSDPPVFDRRSFEAKFQLNWVAR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 10.3%; Score 101; DB 11; Length 132; Local Similarity 25.8%; Pred. No. 8.61e-02; nes 33; Conservative 34; Mismatches 50; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 14; Length 19:
Pred. No. 1.19e-01;
14; Mismatches 17; Indels
                                                                                                                                                                                                                                               STRAIN-FISHER;
MAGNALDO T., DARWON M.;
SUBMITTED (DATA BANKS.
EMBL, AF036941; G2687669; -.
PROSITE; PS00309; LECTIN_GALACTOSIDE; 1.
SEQUENCE 132 AA; 14889 MW; 9BBBC4D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOLOYYEV A.G.;
SUBMITTED (OCT-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 246351; E122444; -.
SEQUENCE 195 AA; 21709 MW; 04D0D3B9 CRC32;
                                                         01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
GALECTIN-7.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                     132 AA
                     PRT;
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083076 PRELIMINARY;
083076 01-NOV-1996 (TREMBLREL. 01, CF
01-NOV-1996 (TREMBLREL. 01, LZ
01-NOY-1998 (TREMBLREL. 07, LZ
BETA-A PROTEIN.
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Best Local Similarity 31.4%;
Matches 16; Conservative
                     PRELIMINARY;
                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
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LT 10
054958
054958;
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Matches
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  RESULT
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MOL. IMMUNOL. 33:101-112(1996).
MOL. IMMUNOL. 33:101-112(1996).
MOL. 147810; G1322034;
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS01009; LDLRA_1; 1.
PRAM; PF000089; trypsin.
PFAM; PF000530; SRCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                  213 KDFILEEALSFTSSHLESLAASGTCPPHLSVRIRNALGLSQHWNMEMLVPVEFIPFYEQE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 RGLVLQEPKHFTVS-LRDQAAHAPVTLRASFADR-TLAWISRWGQKKLISAPFL-FYPQR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
BEVAN M., TERRYN N., ARDILES W., BUYSSHAERT C., DASSEVILLE R., DE CLERCK R., DE KEYSER A., NEYT P., ROUZE P., VAN DEN DAELE H., VILLAROEL R., GIELEN J., VAN MONTAGU M., BANCROFT I., MEWES H.W. MAYER K., SCHUELLER C.; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                          Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 98; DB 11; Length 603; Pred. No. 2.28e-01; 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLORELLA VULGARIS.
EUKARYOTA; PLANTA; PHYCOPHYTA; CHLOROPHYTA (GREEN ALGAE);
CHLOROPHYCEAE; CHLOROCOCCALES; OOCYSTACEAE.
                                                                                                                                                                                                                                                                                                                       Query Match 10.0%; Score 98; DB 10; Length 573
Best Local Similarity 28.2%; Pred. No. 2.28e-01;
Matches 22; Conservative 20; Mismatches 31; Indels
                                                                                                                                                             SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITITED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AL022224; E1283969; -.
SEQUENCE 573 AA; 66617 MW; 21B69D3A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
COMPLEMENT COMPONENT FACTOR I (COMPLEMENT FACTOR I)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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07,
07,
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Best Local Similarity 47.6%;
Matches 10; Conservative
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65 RWGQKKLISAPFLFYPQRFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : :|| | ::||:
83 F-FEVLLL-FQEGGLKLA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C;
MEDLINE; 96175003.
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SEQUENCE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGROBACTERIUM TUMEFACIENS, AND AGROBACTERIUM SP.
PLASMID PIICHRYS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                  ö
                                                                                                                                                                        Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.8%; Score 96; DB 2; Length 295;
Best Local Similarity 36.1%; Pred. No. 4.33e-01;
Matches 26; Conservative 14; Mismatches 26; Indels
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN-CHRY5;
OGER P.M., VAUDEQUIN V., DESSAUX Y.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ANT4;
OGER P.M., VAUDEQUIN-DRANSART V., DESSAUX Y.;
OWENTITED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.EMBL; AF065242; G3153870; -.
EMBL; U67851; G3033355; -.
                                                                                                                                                                                                                                                                                                                                                           LT 15
070110 PRELIMINARY; PRT; 295 AA.
070110 070110,
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
PUTATIVE INNER MEMBRANE PROTEIN CHTI.
CHTI. OR CHTJ.
               TRANSPOSON-ZEPP;
HIGASHIYAMA T., NOTTOSHI Y., FUJIE M., YAMADA T.;
HIGASHIYAMA T., NOTTOSHI Y., FUJIE M., YAMADA T.;
HEMBO J. 16:3715-37211997).
EMBL; BABO08865; D1026697; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1309 AA; 141659 MW; C874E321 CRC32;
                                                                                                                                                                   Score 97; DB 10; Ler
Pred. No. 3.15e-01;
15; Mismatches 11;
                                                                                                                                                                                                                                                       810 KHLGIPLSTQPAAAATALYTAIIEKVEARIARWSGFRL 847
                                                                                                                                                                                                                                                                                SEQUENCE 295 AA; 32054 MW; DD8DEF72 CRC32;
                                                                                                                                                                     Query Match 9.9%;
Best Local Similarity 31.6%;
Matches 12; Conservative
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMID.
                                                                                                                                                                                                                                                                                                                                                                  RESULT
SORTERS
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